

/* CURRENT FILING DATE: 2004-07-16
 /* PRIOR APPLICATION NUMBER: US 60/303, 858
 /* PRIOR FILING DATE: 2001-07-09
 /* PRIOR APPLICATION NUMBER: US10/603, 566
 /* PRIOR FILING DATE: 2003-06-25
 /* PRIOR APPLICATION NUMBER: US 09/905, 253
 /* PRIOR FILING DATE: 2001-07-13
 /* PRIOR APPLICATION NUMBER: US 10/201, 187
 /* PRIOR FILING DATE: 2001-07-23
 /* NUMBER OF SEQ ID NOS: 97
 /* SOFTWARE: PatentIn version 3.1
 /* SEQ ID NO: 61
 /* LENGTH: 9
 /* TYPE: PRT
 /* ORGANISM: Homo sapiens
 US-10-893-485-61

Query Match 100.0%; Score 51; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.7e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 YFPQQFAFS 9
 Db 1 YFPQQFAFS 9

RESULT 3
 US-10-603-566-62
 /* Sequence 62, Application US/10603566
 /* Publication No. US2004008696A1
 /* GENERAL INFORMATION:
 /* APPLICANT: Wittamer, Valerie
 /* COMMUNI, David
 /* APPLICANT: Vandenbogaerde, Ann
 /* APPLICANT: Dethieux, Michel
 /* APPLICANT: Parmentier, Marc
 /* TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
 /* FILE REFERENCE: 9409/2212
 /* CURRENT FILING DATE: 2003-06-25
 /* PRIOR APPLICATION NUMBER: US 60/303, 858
 /* PRIOR FILING DATE: 2001-07-09
 /* PRIOR APPLICATION NUMBER: US 09/905, 253
 /* PRIOR FILING DATE: 2001-07-13
 /* PRIOR FILING DATE: 2001-07-23
 /* NUMBER OF SEQ ID NOS: 91
 /* SOFTWARE: PatentIn version 3.2
 /* SEQ ID NO: 62
 /* LENGTH: 10
 /* TYPE: PRT
 /* ORGANISM: Homo sapiens
 US-10-603-566-62

Query Match 100.0%; Score 51; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.028e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 YFPQQFAFS 9
 Db 2 YFPQQFAFS 10

RESULT 4
 US-10-893-485-62
 /* Sequence 62, Application US/10893485
 /* Publication No. US2005015509A1
 /* GENERAL INFORMATION:
 /* APPLICANT: Wittamer, Valerie
 /* COMMUNI, David
 /* APPLICANT: Vandenbogaerde, Ann
 /* APPLICANT: Dethieux, Michel
 /* APPLICANT: Parmentier, Marc

Query Match 100.0%; Score 51; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.03e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 YFPQQFAFS 9
 Db 3 YFPQQFAFS 11

RESULT 5
 US-10-603-566-85
 /* Sequence 85, Application US/10603566
 /* Publication No. US2004008696A1
 /* GENERAL INFORMATION:
 /* APPLICANT: Wittamer, Valerie
 /* COMMUNI, David
 /* APPLICANT: Vandenbogaerde, Ann
 /* APPLICANT: Dethieux, Michel
 /* APPLICANT: Parmentier, Marc
 /* TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
 /* FILE REFERENCE: 9409/2212
 /* CURRENT FILING DATE: 2003-06-25
 /* PRIOR APPLICATION NUMBER: US 60/303, 858
 /* PRIOR FILING DATE: 2001-07-09
 /* PRIOR APPLICATION NUMBER: US 09/905, 253
 /* PRIOR FILING DATE: 2001-07-13
 /* PRIOR APPLICATION NUMBER: US 10/201, 187
 /* PRIOR FILING DATE: 2001-07-23
 /* NUMBER OF SEQ ID NOS: 91
 /* SOFTWARE: PatentIn version 3.2
 /* SEQ ID NO: 85
 /* LENGTH: 11
 /* TYPE: PRT
 /* ORGANISM: Homo sapiens
 US-10-603-566-85

Query Match 100.0%; Score 51; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.03e+00;
 Matches 9; Conservative 0; Mismatches 0; Indels 0;
 Gaps 0;

Qy 1 YFPQQFAFS 9
 Db 3 YFPQQFAFS 11

RESULT 6
 US-10-893-485-85
 /* Sequence 85, Application US/10893485
 /* Publication No. US2005015509A1
 /* GENERAL INFORMATION:
 /* APPLICANT: Wittamer, Valerie
 /* COMMUNI, David
 /* APPLICANT: Vandenbogaerde, Ann
 /* APPLICANT: Dethieux, Michel
 /* APPLICANT: Parmentier, Marc

APPLICANT: Vandenbogaerde, Ann
 APPLICANT: Detheux, Michel
 APPLICANT: Parmentier, Marc
 TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
 FILE REFERENCE: 9409/2045C
 CURRENT APPLICATION NUMBER: US/10/893,485
 CURRENT FILING DATE: 2004-07-16
 PRIOR APPLICATION NUMBER: US 60/303,858
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US10/603,566
 PRIOR FILING DATE: 2003-06-25
 PRIOR APPLICATION NUMBER: US 09/905,253
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 10/201,187
 PRIOR FILING DATE: 2001-07-23
 NUMBER OF SEQ ID NOS: 97
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 85
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-893-485-85

Query Match 100.0%; Score 51; DB 5; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.03;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9
 Db 3 YFPQQFAFS 11

RESULT 7
 US-10-603-566-63
 Sequence 63, Application US/10603566
 Publication No. US20040086966A1
 GENERAL INFORMATION:
 APPLICANT: Wittamer, Valerie
 APPLICANT: Communi, David
 APPLICANT: Vandenbogaerde, Ann
 APPLICANT: Detheux, Michel
 APPLICANT: Parmentier, Marc
 TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
 FILE REFERENCE: 9409/2212
 CURRENT APPLICATION NUMBER: US/10/603,566
 CURRENT FILING DATE: 2003-06-25
 PRIOR APPLICATION NUMBER: US 60/303,858
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US 09/905,253
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 10/201,187
 PRIOR FILING DATE: 2001-07-23
 NUMBER OF SEQ ID NOS: 91
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 63
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-603-566-63

Query Match 100.0%; Score 51; DB 4; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.033;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9
 Db 4 YFPQQFAFS 12

RESULT 8
 US-10-893-485-63
 Sequence 63, Application US/10893485
 Publication No. US20050155090A1
 GENERAL INFORMATION:
 APPLICANT: Wittamer, Valerie
 APPLICANT: Communi, David
 APPLICANT: Vandenbogaerde, Ann
 APPLICANT: Detheux, Michel
 APPLICANT: Parmentier, Marc
 TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
 FILE REFERENCE: 9409/2045C
 CURRENT APPLICATION NUMBER: US/10/893,485
 CURRENT FILING DATE: 2004-07-16
 PRIOR APPLICATION NUMBER: US 60/303,858
 PRIOR FILING DATE: 2001-07-09
 PRIOR APPLICATION NUMBER: US 09/905,253
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 10/201,187
 PRIOR FILING DATE: 2001-07-23
 NUMBER OF SEQ ID NOS: 97
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 63
 LENGTH: 12
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-893-485-63

Query Match 100.0%; Score 51; DB 4; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.036;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9
 Db 5 YFPQQFAFS 13

RESULT 10

US-10-893-485-64 ; Sequence 64, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; COMMUNI, David
; APPLICANT: Vandenbergaele, Ann
; DETHEU, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/89
; CURRENT FILING DATE: 2004-07-16
; PRIORITY APPLICATION NUMBER: US 60/303,
; PRIORITY FILING DATE: 2001-07-09
; PRIORITY APPLICATION NUMBER: US10/603,5
; PRIORITY FILING DATE: 2003-06-25
; PRIORITY APPLICATION NUMBER: US 09/905,
; PRIORITY FILING DATE: 2001-07-13
; PRIORITY APPLICATION NUMBER: US 10/201,
; PRIORITY FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: Patent in version 3.1
; SEQ ID NO: 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-893-485-64

Qy	Db	YFPGGFAFS 9	YFPGGFAFS 13
Query Match	100.0%	Score 51;	Score 51;
Best Local Matches	100.0%	Pred. No. 0.036;	Length 13;
Similarity	9;	Mismatches 0;	Indels 0;
Conservative			

```

RESULT 11                               US-10-603-566-84
; Sequence 84, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
;   APPLICANT: Wittamer, Valerie
;   APPLICANT: Communi, David
;   APPLICANT: Vandembogaerde, Ann
;   APPLICANT: Dethieux, Michel
;   APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and
; FILE REFERENCE: 9405/2212
; CURRENT APPLICATION NUMBER: US/10/65
; CURRENT FILING DATE: 2003-06-25
; PRIORITY APPLICATION NUMBER: US 60/303
; PRIORITY FILING DATE: 2001-07-09
; PRIORITY APPLICATION NUMBER: US 09/905
; PRIORITY FILING DATE: 2001-07-13
; PRIORITY APPLICATION NUMBER: US 10/201
; PRIORITY FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-84

Query Match                           100.0% ; Score: 9
Best Local Similarity 100.0% ; Precision: 0, Mismatches: 9
Matches 9; Conservative 9
Db
Qy      1 YFPGQFAFS 9
      7 YFPGQFAFS 15

```

RESULT 12

US-10-693-485-84

Sequence 84, Application US/10893485

Publication No. US20050155090A1

GENERAL INFORMATION:

APPLICANT: Wittamer, Valerie

APPLICANT: Communi, David

APPLICANT: Vandenoever, Ann

APPLICANT: Dethieux, Michel

APPLICANT: Parmentier, Marc

TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR

FILE REFERENCE: 9439/2045C

CURRENT APPLICATION NUMBER: US/10/693,485

CURRENT FILING DATE: 2004-07-16

PRIOR APPLICATION NUMBER: US 60/303,858

PRIOR FILING DATE: 2001-07-09

PRIOR APPLICATION NUMBER: US10/603,566

PRIOR FILING DATE: 2003-06-25

PRIOR APPLICATION NUMBER: US 09/905,253

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 10/201,187

PRIOR FILING DATE: 2001-07-23

NUMBER OF SEQ ID NOS: 97

SOFTWARE: PatentIn version 3.1

SEQ ID NO 84

LENGTH: 15

TYPE: seq

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; ORGANISM: Homo sapiens
US-10-893-485-84

Query Match          100.0%;  Score 51;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 0.041;
Matches 9;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
Qy          1 YFPQQFARS 9
Db          7 YFPQQFARS 15

```

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RESULT 13
US-10-603-566-83
; Sequence 83, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; COMMUNICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Dethieux, Michel
; APPLICANT: Parmentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin Receptor
; FILE REFERENCE: 9409/2212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 83
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-603-566-83
; Score 51; DB 4; Length 17;
; Query Match 100.0%; Pred. No. 0.046%; Indels 0; Gaps 0;
; Best Local Similarity 100.0%; Mismatches 0; Conservative 0; Matches 9;

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Qy 1 YFPQQFAFS 9
Db 9 YFPQQFAFS 17

RESULT 14
US-10-893-485-83
; Sequence 83, Application US/10893485
; Publication No. US20050155090A1
GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of ChemerinR
FILE REFERENCE: 9409/2045C
CURRENT APPLICATION NUMBER: US/10/893,485
PRIORITY NUMBER: US 60/303,858
PRIOR FILING DATE: 2004-07-16
PRIOR APPLICATION NUMBER: US10/603,566
PRIOR FILING DATE: 2003-06-25
PRIOR APPLICATION NUMBER: US 09/905,253
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 10/201,187
PRIOR FILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 97
SOFTWARE: Patentin version 3.1
SEQ ID NO: 83
LENGTH: 17
TYPE: PRT
ORGANISM: Homo sapiens
US-10-893-485-83

Query Match 100.0%; Score 51; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.046; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9
Db 9 YFPQQFAFS 17

RESULT 15
US-09-905-253A-31
; Sequence 31, Application US/0905253A
; Publication No. US20030096299A1
GENERAL INFORMATION:
; APPLICANT: Wittamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenbogaerde, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parmentier, Marc
TITLE OF INVENTION: Natural Ligand of G Protein Coupled Receptor ChemR23 and Uses The
CURRENT APPLICATION NUMBER: US/09/905,253A
CUTRRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: US 60/303,858
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.0
SEQ ID NO: 31
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-253A-31

Query Match 100.0%; Score 51; DB 3; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.049; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9

Result No.	Score	Query	Match	Length	DB ID	Description
<hr/>						
1	51	100.0	163	2	US-09-949-016-6284	Sequence 6284, AP
2	51	100.0	166	2	US-09-949-016-11175	Sequence 11175, A
3	37	72.5	363	2	US-09-270-767-44161.	Sequence 44161, A
4	37	72.5	422	2	US-09-94-016-8167	Sequence 8167, AP
5	37	72.5	483	2	US-09-248-796A-20218	Sequence 20218, A
6	37	72.5	509	1	US-08-890-980-2	Sequence 2, Appli
7	37	72.5	509	2	US-08-890-979-2	Sequence 2, Appli
8	37	72.5	509	2	US-09-031-894-2	Sequence 2, Appli
9	37	72.5	509	2	US-09-031-626-2	Sequence 2, Appli
10	37	72.5	509	2	US-09-052-725-59	Sequence 59, Appli
11	36	70.6	909	2	US-09-053-092-1315	Sequence 1315, AP
12	36	70.6	1326	2	US-09-480-039A-7584	Sequence 7584, AP
13	36	70.6	1330	2	US-09-54-681A-8057	Sequence 8057, AP
14	35	68.6	311	1	US-08-19-802A-164	Sequence 164, APP
15	35	68.6	311	2	US-08-477-346-16	Sequence 164, APP
16	35	68.6	311	2	US-08-477-089-164	Sequence 164, APP
17	35	68.6	311	2	US-08-48-072A-164	Sequence 164, APP
18	35	68.6	255	2	US-09-90-540-12488	Sequence 12488, A
19	35	68.6	341	1	US-08-19-802A-45	Sequence 45, APP
20	35	68.6	341	2	US-08-477-346-45	Sequence 45, APP
21	35	68.6	341	2	US-08-473-089-45	Sequence 45, APP
22	34	68.6	341	2	US-08-47A-45	Sequence 45, APP
23	34	66.7	256	2	US-09-248-796A-2026	Sequence 2026, A
24	34	66.7	1299	2	US-09-232-991A-31121	Sequence 31121, A
25	33	64.7	20	2	US-09-993-433-26	Sequence 214, APP
26	33	64.7	121	2	US-10-014-012-214	Sequence 213, APP
27	33	64.7	122	2	US-10-014-012-213	Sequence 213, APP

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; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NO: 11175
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11175

Query Match 100.0%; Score 51; DB 2; Length 166;
Best Local Similarity 100.0%; Pred. No. 0.052; 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPQGQAFS 9
Db 152 YFPQGQAFS 160

RESULT 3
US-09-270-767-44161
Sequence 44161, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 44161
LENGTH: 363
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-44161

Query Match 72.5%; Score 37; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 46; 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPQGQF 6
Db 27 YFPQQF 32

RESULT 4
US-09-949-016-8167
Sequence 8167, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL0001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 8167
TYPE: PRT
ORGANISM: Human
US-09-949-016-8167

Query Match 72.5%; Score 37; DB 2; Length 422;
Best Local Similarity 75.0%; Pred. No. 53; 2; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YFPQGQAF 8
Db 262 YFPQMFPP 269

RESULT 5
US-09-248-796A-20218
Sequence 20218, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO: 20218
LENGTH: 483
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20218

Query Match 72.5%; Score 37; DB 2; Length 483;
Best Local Similarity 66.7%; Pred. No. 62; 2; Mismatches 1; Indels 0; Gaps 0;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFPQGQAFS 9
Db 399 YFPQFSVS 407

RESULT 6
US-08-890-980-2
Sequence 2, Application US/08890980
Patent No. 5998441
GENERAL INFORMATION:
APPLICANT: Action, Susan L.
TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HARG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,980
FILING DATE: 10-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MIA-005.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 509 amino acids
TYPE: amino acid
TOPOLOGY: linear

```

MOLECULE TYPE: protein
 US-08-890-980-2

Query Match 72.5%; Score 37; DB 1; Length 509;
 Best Local Similarity 75.0%; Pred. No. 65;
 Matches 6; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0; Gaps 0;

Qy 1 YFPQGQAF 8
 Db 194 YFPGMFPF 201

RESULT 7
 US-08-890-979-2
 / Sequence 2, Application US/08890979
 / Patent No. 6030778

GENERAL INFORMATION:
 / APPLICANT: Action, Susan L.
 / APPLICANT: Ordovas, Jose M.
 / TITLE OF INVENTION: DIAGNOSTIC ASSAYS AND KITS FOR BODY MASS
 / NUMBER OF SEQUENCES: 75
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: FOLLY, HOAG & ELIOT LLP
 / STREET: One Post Office Square
 / CITY: Boston
 / STATE: MA
 / COUNTRY: USA
 / ZIP: 02109-2170
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/890,979
 / FILING DATE: 10-JUL-1997
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Arnold, Beth E.
 / REGISTRATION NUMBER: 35,430
 / REFERENCE/DOCKET NUMBER: MIA-005.02
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 617-832-1000
 / TELEFAX: 617-832-7000
 / INFORMATION FOR SEQ ID NO: 2:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 509 amino acids
 / TYPE: amino acid
 / TOPOLOGY: linear
 / MOLECULE TYPE: Protein
 US-08-890-979-2

Query Match 72.5%; Score 37; DB 2; Length 509;
 Best Local Similarity 75.0%; Pred. No. 65;
 Matches 6; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0; Gaps 0;

Qy 1 YFPQGQAF 8
 Db 194 YFPGMFPF 201

RESULT 8
 US-09-032-894-2
 / Sequence 2, Application US/09032894
 / Patent No. 6130041

GENERAL INFORMATION:
 / APPLICANT: Action, Susan L.
 / TITLE OF INVENTION: SR-B1 NUCLEIC ACIDS AND USES THEREFOR
 / FILE REFERENCE: MIA-005.03
 / CURRENT APPLICATION NUMBER: US/09/032,894
 / CURRENT FILING DATE: 1998-02-27
 / EARLIER APPLICATION NUMBER: 08/890,980

Query Match 72.5%; Score 37; DB 2; Length 509;
 Best Local Similarity 75.0%; Pred. No. 65;
 Matches 6; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0; Gaps 0;

Qy 1 YFPQGQAF 8
 Db 194 YFPGMFPF 201

RESULT 9
 US-09-031-626-2
 / Sequence 2, Application US/09031626
 / Patent No. 6228581

GENERAL INFORMATION:
 / APPLICANT: Action, Susan L.
 / APPLICANT: Ordovas, Jose M.
 / TITLE OF INVENTION: CARDIOVASCULAR ASSAYS AND KITS FOR BODY MASS AND
 / NUMBER OF SEQUENCES: 121
 / FILE REFERENCE: MIA-005.04
 / CURRENT APPLICATION NUMBER: US/09/031,626
 / CURRENT FILING DATE: 1998-02-27
 / EARLIER APPLICATION NUMBER: 08/890,979
 / EARLIER FILING DATE: 1997-07-10
 / NUMBER OF SEQ ID NOS: 121
 / SEQ ID NO: 2
 / LENGTH: 509
 / TYPE: PRT
 / ORGANISM: Human
 US-09-031-626-2

Query Match 72.5%; Score 37; DB 2; Length 509;
 Best Local Similarity 75.0%; Pred. No. 65;
 Matches 6; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0; Gaps 0;

Qy 1 YFPQGQAF 8
 Db 194 YFPGMFPF 201

RESULT 10
 US-09-054-272-59
 / Sequence 59, Application US/09054272

GENERAL INFORMATION:
 / Patent No. 662909

APPLICANT: Lander, Eric S.
 / APPLICANT: Daley, George Q.
 / APPLICANT: Carbill, Michael
 / APPLICANT: Ireland, James S.
 / APPLICANT: Rozen, Steven G.
 / TITLE OF INVENTION: CODING SEQUENCE POLYMORPHISMS
 / NUMBER OF SEQUENCES: 59
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 / STREET: Two Militia Drive
 / CITY: Lexington
 / STATE: MA
 / COUNTRY: USA
 / ZIP: 02173

COMPUTER READABLE FORM:
 / MEDIUM TYPE: Diskette
 / COMPUTER: IBM Compatible
 / OPERATING SYSTEM: Windows 95

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; SOFTWARE: FastSEO for Windows Version 2.0b
; CURRENT APPLICATION DATA: US/09/054,272
; FILING DATE: 01-APR-1998
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: WHI98-05
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-161-6740
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 509 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-054-272-59

Query Match 72.5%; Score 37; DB 2; Length 509;
Best Local Similarity 75.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 YFPQQFAF 8
Db 194 YFPGMFPP 201

RESULT 11
US-09-538-092-1315
; Sequence 1315; Application US/09538092
; Parent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapateqFormatter Version 0.9
; SEQ ID NO: 1315
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (0) (0)
; OTHER INFORMATION: Polypeptide Accession Number Q14028
US-09-538-092-1315

Query Match 70.6%; Score 36; DB 2; Length 909;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 YFPQQFAF 9
Db 523 YFPGVFPP 531

RESULT 12
US-09-489-039A-7584

; Sequence 7584; Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709-2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO: 7584
; LENGTH: 1326
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7584

Query Match 70.6%; Score 36; DB 2; Length 1326;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFPQQFAF 8
Db 509 YFPQYEF 516

RESULT 13
US-09-543-681A-8057
; Sequence 8057; Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709-1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO: 8057
; LENGTH: 1330
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8057

Query Match 70.6%; Score 36; DB 2; Length 1330;
Best Local Similarity 62.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YFPQQFAF 8
Db 508 YFPQYEF 515

RESULT 14
US-08-190-802A-164
; Sequence 164; Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
; APPLICANT: Mochly-Rosen, Daria
; APPLICANT: Ron Dorit
; TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: P.O. Box 60550
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306-0850
US-09-489-039A-7584

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190, 802A
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Fabian, Gary R.
; REGISTRATION NUMBER: 33, 875
; REFERENCE/DOCKET NUMBER: 8600-0139
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0980
; TELEFAX: (415) 324-0960
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: GTP binding prt squid rIV, Fig. 28
; US-08-190-802A-164

Query Match      68.6%; Score 35; DB 1; Length 31;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy      1 YFPQGFAFS 9
Db      11 YFPNGFAFA 19

Search completed: December 2, 2005, 05:58:30
Job time : 48 secs

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477, 346
; FILING DATE: 01-FEB-1994
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/487, 072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29, 959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763

; INFORMATION FOR SEQ ID NO: 164:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: Peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: GTP binding prt squid rIV, Fig. 28
; US-08-477-346-164

Query Match      68.6%; Score 35; DB 2; Length 31;
Best Local Similarity 66.7%; Pred. No. 7.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy      1 YFPQGFAFS 9
Db      11 YFPNGFAFA 19

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477, 346
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/487, 072
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MORASHIGE, KATE H.
; REGISTRATION NUMBER: 29, 959
; REFERENCE/DOCKET NUMBER: 2550-0025.20
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763

```

- All of the sequence databases on ABS have recently been updated.
- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein archive database (UniPARC) at: <http://www.pir.uniprot.org/database/archive.shtml>
- If you have any questions regarding this information or your results, please contact any STC searcher.
- When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

Scoring table:	BLOSUM62	ALIGMENTS					
Gapop:	10.0	Gapext 0.5					
Searched:	2166443 seqs, 705528306 residues						
Total number of hits satisfying chosen parameters:	2166443						
Minimum DB seq length:	0						
Maximum DB seq length:	2000000000						
Post-processing:	Minimum Match 0*						
	Maximum Match 100*						
	Listing first 45 summaries						
Database :	UniProt 05-80:*						
	1: uniprot_sprot;*						
	2: uniprot_trembl;*						
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
		SUMMARIES					
Result No.	Score	Query	Match	Length	DB	ID	Description
1	51	100.0	163	1	TIG2_HUMAN	Q99699	homo sapien
2	51	100.0	163	1	TIG2_PONGO	Q5251	pongo pygmaeus
3	51	100.0	163	2	TIG2_HUMAN	Q7602	homo sapien
4	47	92.2	163	1	TIG2_CRICETULUS	Q8BQ8	criceetus
5	47	92.2	163	1	TIG2_RAT	Q5BK77	rattus norvegicus
6	44	86.3	1316	2	Q7MRA1_WOLVISU	Q7MRA1	wolinella s.
.7	42	82.4	500	2	Q989D1_RHILIO	Q989D1	rhizobium 1
8	41	80.4	162	1	TIG2_MOUSE	Q9Ad06	mus-musculus
9	37	72.5	186	2	Q516H6_ENTHII	Q516H6	entomoeba h.
10	37	72.5	227	2	Q6FFM5_ACETAD	Q6FFM5	acinetobacter
11	37	72.5	258	2	Q7NA59_MCGA	Q7NA59	mycoplasma
12	37	72.5	267	2	Q8SV77_ENCCU	Q8SV77	encephalito
13	37	72.5	276	2	Q7NY09_CIRVO	Q7NY09	chrenobacter
14	37	72.5	338	2	Q9SUG3_ARATH	Q9SUG3	arabidopsis
15	37	72.5	341	2	Q7QCL7_ANOGA	Q7QCL7	anophelis gambiae
16	37	72.5	342	2	Q8SYT1_DROME	Q8SYT1	drosophila
17	37	72.5	342	2	Q9W0U5_DROME	Q9W0U5	drosophila
18	37	72.5	509	2	Q52L25_HUMAN	Q52L25	homo sapien
19	37	72.5	552	1	SCRBL1_HUMAN	SCRBL1	homo sapien
20	37	72.5	564	2	Q5A1A8_CANAL	Q5A1A8	candida albicans
21	37	72.5	569	2	Q6BUT6_DEBHA	Q6BUT6	debaryomyces
22	37	72.5	581	2	Q59FM4_HUMAN	Q59FM4	homo sapien
23	37	72.5	636	2	Q87D11_XYLIFT	Q87D11	xylophila
24	37	72.5	636	2	Q9dc18_XYLIFA	Q9dc18	xylophila
25	36	70.6	147	2	Q9PNK1_RAT	Q9PNK1	rattus norvegicus
26	36	70.6	211	2	Q5X5V3_LEPSEA	Q5X5V3	leptospira
27	36	70.6	248	2	Q4ZN30_PSESY	Q4ZN30	pseudomonas
28	36	70.6	248	2	Q88AH9_PSESM	Q88AH9	pseudomonas
29	36	70.6	342	2	Q4J8W1_SULACN	Q4J8W1	sulfolobus
30	36	70.6	378	2	Q5Lg99_BACFCR	Q5Lg99	bacteroides
31	36	70.6	378	2	Q64Nj9_BACFR	Q64Nj9	bacteroides

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL CC -!- SUBCELLULAR LOCATION: Secreted (Potential).

CC -!- TISSUE SPECIFICITY: Highly expressed in skin (basal and suprabasal layers of the epidermis, hair follicles and endothelial cells).

CC Also found in pancreas, liver, spleen, prostate, ovary, small intestine and colon.

CC -!- INDUCTION: Inhibited in psoriatic lesions. Activated by tazarotene in skin rashes and in the epidermis of psoriatic lesions.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC DR EMBL; U77594; AB47975_1; -; mRNA.

CC DR EMBL; BC000632; BAA76499_1; -; mRNA.

CC DR EMBL; BC000669; AAH00069_1; -; mRNA.

CC DR Ensemble; ENSG00000106538; Homo sapiens.

CC DR H-InvDB; HIX0007202; -.

CC DR MIM; 601973; -.

CC DR GO; GO:0001523; P:retinoid metabolism; IDA.

CC KW Signal.

CC PT SIGNAL 1 16 Potential.

CC FT CHAIN 17 163 Retinoic acid receptor responder protein

CC SEQUENCE 18618 MW; A96EB7D099EC3DB CRC64;

CC SQ 163 AA; 100.0%; Score 51; DB 1; Length 163;

CC Query Match 100.0%; Pred. No. 0.091; Gaps 0;

CC Best Local Similarity 100.0%; Matches 9; Conservative 0; Indels 0; Gaps 0;

CC Name=RARRES2;

CC OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

CC OC NCBI_TAXID=9606;

CC OX [1] _NUCLEOTIDE_SEQUENCE.

CC DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

CC RA Hillion L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H., Wagner-McPherson C., Layman D., Maas J., Jeger S., Walker R., Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E., Fewell G.A., Delehaunty K.D., Miner T.L., Nash W.E., Cordes M., Du H., Sun H., Edwards J., Bradshaw Corruth H., Ali J., Andrews S., Isaak A., Vanbrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J., Ozersky P., Bielicki L., Scott K., Holmes R., Harris A., Strong C.M., Hou S., Tonlinson C., Dauphin-Kohlberg S., Kozlowski-Reilly A., Leonard S., Rohling T., Rock S.M., Tint-Wollam A.-M., Abbott A., Minx P., Maupin R., Strowmatt C., Latraille P., Miller N., Johnson D., Murray J., Woesner J. P., Wendl M.C., Yang S.-P., Schulz B.R., Wallis J.W., Spleeth J., Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L., Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R., Clifton S.W., Chissoe S.L., Marra M.A., Raymond C., Haugen B., Gillett W., Zhou Y., James R., Phelps K., Iadanoto S., Bubb K., Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Furey T.S., Baertsch R.A., Brent R., Keibler E., Flicek P., Bork P., Gish W.R., Bailey J.A., Portnoy M.B., Torrents D., Chinnaiyan A.T., Green E.D., Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green B.D., Waterston R.H., Wilson R.K.; RT "The DNA sequence of human chromosome 7.";

CC DR Nature 424:157-164(2003).

CC RN [2] _NUCLEOTIDE_SEQUENCE.

CC RA Le T., Ozersky P., Stoneking T., Wohldmann P.;

CC RL [3] _NUCLEOTIDE_SEQUENCE.

CC RN [4] _NUCLEOTIDE_SEQUENCE.

CC RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

CC RN [5] _NUCLEOTIDE_SEQUENCE.

CC RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.

CC RN [6] _NUCLEOTIDE_SEQUENCE.

CC RL Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

CC RN [7] _NUCLEOTIDE_SEQUENCE.

CC RL Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

CC RN [8] _NUCLEOTIDE_SEQUENCE.

CC RL Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.

CC -!- SUBCELLULAR LOCATION: Secreted (Potential).

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CC DR EMBL; CR861021; CAH93115_1; -; mRNA.

CC KW Signal.

CC PT CHAIN 1 20 Potential.

CC PT CHAIN 21 163 Retinoic acid receptor responder protein

CC SQ 163 AA; 100.0%; Score 51; DB 1; Length 163;

CC DR EMBL; AC005586; AAS010384_1; -; Genomic_DNA.

CC DR EMBL; CR541992; CAG46789_1; -; mRNA.

Query Match 100.0%; Score 51; DB 1; Length 163;

Best Local Similarity 100.0%; Pred. No. 0.091; Gaps 0;

Matches 9; Conservative 0; Indels 0; Gaps 0;

Name=RARRES2;

OS Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Buteraria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TAXID=9606;

OX [1] _NUCLEOTIDE_SEQUENCE.

OX DR MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

ID QTLE02_HUMAN PRELIMINARY;

AC QTLE02;

DT 10-MAY-2005 (TREMBL); 30, Created)

DT 10-MAY-2005 (TREMBL); 30, Last sequence update)

DT 10-MAY-2005 (TREMBL); 30, Last annotation update)

DE HYPOTHETICAL protein RARRES2.

DE Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost

DR	EMBL: CR542026; CAG46023.1; - ; mRNA.	OC	Muridae; Murinae; <i>Rattus</i> .
KW	Hypothetical protein.	OX	NCBI_TaxID=10116;
SEQUENCE	163 AA; 18617 MW; A96EE7D0999EBC3DB CRC64;	RN	[1] _NUCLEOTIDE SEQUENCE.
Query Match	100.0%; Score 51; DB 2; Length 163;	RC	TISSUE=Liver;
Best Local Similarity	100.0%; Pred. No. 0.091; 0; Mismatches 0; Indels 0; Gaps 0;	RX	Medline=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Matches 9; Conservative 0;		RA	Stratensberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Qy	1 YFPQGQFAPS 9	RA	Klaasner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D.,
Db	149 YFPQGQFAPS 157	RA	Altachul S.P., Zeeberg B., Buerow K.H., Bhat N.K.,
		RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
		RA	Diatchenko L., Marusina A., Farmer A.A., Rubin G.M., Hong L.,
		RA	Stapleton M., Soares M.B., Bonaldo M.F., Cesavant T.L., Scheetz T.E.,
		RA	Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
		RA	Raha S.S., Logueblano N.A., Carninci P., Mullahy S.J.,
		RA	Bosak S.A., McEwan P.J., Peters G.J., Abramson K.J., Malek J.A., Gunaratne P.H.,
		RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
		RA	Villalon D.K., Murany D.M., Soderren B.J., Lu X., Gibbs R.A.,
		RA	Faley J., Heitton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
		RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
		RA	Blakesley R.W., Touchman J.W., Schmitz J., Dickson M.C.,
		RA	Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M.,
		RA	Butterfield V.S.N., Krzywinski M.I., Skalbka U., Smailus D.E.,
		RA	Schnarch A., Schein J.S., Jones S.J.M., Marrs M.A.,
		RA	"Generation and initial analysis of more than 15,000 full-length human
		RT	RT and mouse cDNA sequences.";
		RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
		RN	[2]
		RP	NUCLEOTIDE SEQUENCE.
		RC	TISSUE=Liver;
		RG	NIH MGC Project;
		RL	Submitted (NMR-2005) to the EMBL/GenBank/DBJ databases.
		DR	EMBL; BC091177; AAH91177.1; - ; mRNA.
		KW	Receptor.
		SQ	SEQUENCE 163 AA; 18504 MW; A2D496F29F2D1BEE CRC64;
		Query	Match Score 47; DB 2; Length 163;
		Best	Local Similarity 98.9%; Pred. No. 0.55%;
		Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	
		Qy	1 YFPQGQFAPS 9
		Db	: 149 FFPPQFAPS 157
		RESULT	6
		Q7MR17_WOLSU	Q7MR17_WOLSU PRELIMINARY; PRT; 1316 AA.
		ID	Q7MR17_WOLSU PRELIMINARY; PRT; 1316 AA.
		AC	Q7MR17_WOLSU PRELIMINARY; PRT; 1316 AA.
		DT	01-MAR-2004 (TREMBLrel. 26, Created)
		DT	01-MAR-2004 (TREMBLrel. 26, Last sequence update)
		DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
		DE	Hypothetical protein.
		GN	OrderidocNames=WS197;
		OS	Wolinella succinogenes.
		OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
		OX	Helicobacteraceae; Wolinella.
		NCBI_TaxID=44;	
		RN	[1] _NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
		RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
		RC	STRAIN=DSMZ 1740;
		RX	Medline=223882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
		RA	Baar C., Eppinger M., Radatz G., Simon J., Lanz C., Klimmek O.,
		RA	Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
		RA	Meyer F., Lederer H., Schuster S., C.;
		RA	"Complete genome sequence and analysis of <i>Wolinella succinogenes</i> ."
		RT	Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695 (2003).
		DR	EMBL; BX571661; CAE10815.1; - ; Genomic DNA.
		DR	GO; GO:1005727; C:extrachromosomal circular DNA; IEA.
		DR	InterPro; IPR01434; DUF11.
		DR	TIGRFAMs; TIGR01451; B:ant repeat; 1.
		KW	Complete proteome; Hypothetical protein.
		SQ	SEQUENCE 1316 AA; 141999 MW; 48861B121C5E46EO CRC64;
		Qy	1 YFPQGQFAPS 9
		Db	: 149 FFPPQFAPS 157
		RESULT	5
		Q5BK77_RAT	Q5BK77_RAT PRELIMINARY;
		ID	Q5BK77_RAT PRELIMINARY;
		AC	Q5BK77_RAT PRELIMINARY;
		DT	10-MAY-2005 (TREMBLrel. 30, Created)
		DT	10-MAY-2005 (TREMBLrel. 30, Last sequence update)
		DT	10-MAY-2005 (TREMBLrel. 30, Last annotation update)
		DE	Retinoic acid receptor responder (Tazarotene induced) 2 (Predicted).
		GN	Name=Retros predicted.
		OS	Rat; Rattus norvegicus (Rat).
		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Euarchontoglires; Glires; Rodentia; Sciurognathi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Query Match 86.3%; Score 44; DB 2; Length 1316;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9
Db 579 YFPGLFAFS 587

RESULT 7
Q989D1_RHIL0 ID Q989D1_RHIL0 PRELIMINARY; PRT; 500 AA.
DT 01-OCT-2001 (TRIMBLrel. 18, Created)
DT 01-MAR-2002 (TRIMBLrel. 20, Last annotation update)
DE M16478 protein.
GN OrderedLocusNames=m16478;
OS Rhizobium loti (Mesorhizobium loti)
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MAFF103093;
RX MEDLINE=21082930; PubMed=11214968;
RA Nakamura T., Nakamura Y., Asanizu S., Kato T., Sasamoto S.,
RA Watanabe A., Iida Sawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki C., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338 (2000).
DR EMBL; BA000012; BAB52766.1; -; Genomic_DNA.
KW Complete proteome;
SEQUENCE 500 AA; 53233 MW; 117D88E418223ASF CRG64;

Query Match 82.4%; Score 42; DB 2; Length 500;
Best Local Similarity 87.5%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPQQFAF 8
Db 236 YFPGNFAF 243

RESULT 8
TIG2_MOUSE ID TIG2_MOUSE STANDARD; PRT; 162 AA.
AC Q9DD06; Q8CRH0;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Retinoic acid receptor responder protein 2 precursor.
GN Name=Rarres2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathia;
OC Muroidea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=223545683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Kiyosawa H.,
RA Niikido I., Osato N., Saito R., Suzuki H., Yamakawa I., Gojobori T.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuoka H., Batalov S., Beise K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dragani T.A., Fletcher C.F., Forrest A., Frzer K.S.,
RA Gaasterland T., Garibaldi M., Gissi C., Godzik A., Gough J.,

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Kongaya A., Kurokawa T.V., Lee Y., Lenhard B., Lyons P.A.,
RA Magliocca D.R., Maltais L., Marchionni L., Miki H., Pesole G.,
RA Nagashima T., Numata K., Okido T., Pavon W.J., Pertea G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reid D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setcov M., Shimada K.,
RA Sultana R., Teknsta Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wildling L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Nakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Arakawa K., Fukuda S.,
RA Hara A., Hashizume W., Imotori K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs";
RT Nature 420:563-573 (2002).
RL RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT PHB-3.
RC STRAIN=FVB/N; TISSUE=Liver;
RX MEDLINE=2238457; PubMed=12479732; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klaauwer R.D., Collins F.S., Wagner L., Shearer C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan D., Moore T., Max S.I., Wang J., Hsieh F.,
RA Ditchkenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., McDonald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uscio T.B., Tobiishi K., Carninci P., Pratige C.,
RA Blaustein M.J., Uscio T.B., Tobiishi K., Carninci P., Pratige C.,
RA Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahay S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley S., Hale S.A., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalob D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heilton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,
RA Schnerr A., Schein J.E., Jones S.J.M., Marrs M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL CC -1- SUBCELLULAR LOCATION: Secreted (Potential).

CC CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC DR AK002298; BAB21997.1; -; mRNA.
DR EMBL; BC0388914; AAH18914.1; -; mRNA.
DR Ensembl; ENSMUSG000092901; Mus musculus.
DR MGI; MGI:1918910; Rarres2.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR001894; Cathelicidin.
DR ProDom; PPD01838; Cathelicidin.
DR Polymorphism; Signal.
KW SIGNAL 1 19 Potential.
FT CHAIN 20 162 Retinoic acid receptor responder protein
FT FT 2. -
FT VARIANT 3 3 C → F (in strain FVB/N);
SQ SEQUENCE 162 AA; 18350 MW; 56FD54B1BF16783 CRC64;
Query Match 80.4%; Score 41; DB 1; Length 162;
Best Local Similarity 77.8%; Pred. No. 8.1; Indels 0; Gaps 0;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9
Db ||||| |||||
||| |||||
1 YFPQQFAFS 9

RT	"Genome sequence and gene compaction of the eukaryote parasite Encephalitozoon cuniculi.";	Qy	1 YFPQOF 6
RT	Encephalitozoon cuniculi.;	Db	149 YFPQOF 154
RL	Nature 414:150-153 (2001).		
DR	EMBL; AL590446; CAD2517.1; -; Genomic DNA.		
DR	GO; GO:0004519; F:endonuclease activity; IEA.		
DR	GO; GO:0016787; F:hydrolase activity; IEA.		
DR	InterPro; IPR00042; Intern endonuc.		
DR	PROSITE; P850819; INTEIN ENDONUCLEASE; 1.		
RW	Complete proteome; Hypothetical protein; ENDONUCLEASE; 1.		
SEQUENCE	SEQUENCE 267 AA; 30758 MW; D9E498F499AF639 CRC64;		
Query Match	Score 37; DB 2; Length 267;		
Best Local Similarity	75.0%; Pred. No. 82;		
Matches	6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
Qy	1 YFPQQFAF 8		
Db	: 165 YFPQQFAF 172		
RESULT 13			
Q7NY09 CHRYVO PRELIMINARY;	PRT; 276 AA.		
ID Q7NY09_-			
AC Q7NY09;			
DT 01-MAR-2004 (TREMBLrel. 26, Created)			
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)			
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE Hypothetical protein.			
OrderdLocusNames=CV1467;			
OS Chromobacterium violaceum,			
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC Neisseriaceae; Chromobacterium.			
OC NCBI_TAXID=536;			
RN [1]			
RP NUCLEOTIDE SEQUENCE.			
RC STRAIN=ATCC 12472 / DSM 30191;			
RC MEDLINE=22882880; PubMed=4500782; DOI=10.1073/pnas.1832124100;			
RC Vasconcelos A.T.R., Almeida F.C., Hungria D.F., Almeida L.G.P., de Almeida R.,			
RA Antonio R.V., Almeida F.C., Hungria D.F., Guimaraes C.T.,			
RA Alves-Gomes J.A., Andrade E.M., de Araujo M.F.F.,			
RA Astolfo-Filho S., Araripe J.J., Baptista A.J.J., Bataus L.A.M.,			
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,			
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Buriti H.A.,			
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carrasco D.M.,			
RA Carvalho C.M.B., Cascudo J.C.M., Cavada B.S., Chueire L.M.O.,			
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,			
RA Fantinatti F., Farias I.P., Feijipe R.S., Ferrari L.P., Ferro J.A.,			
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,			
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangheiro T.B.,			
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,			
RA Leão L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,			
RA Madeira H.M.P., Manfio G.P., Maranhão A.Q., Martins W.S.,			
RA di Mairo S.M.Z., de Medeiros S.R.P., Meissner R.V., Moreira M.A.M.,			
RA Nascimento F.P., Nicolas M.F., Oliveira J.G., Oliveira S.C.,			
RA Paixao R.P.C., Parente J.A., Pedroso F.O., Peña S.D.J., Pereira J.O.,			
RA Pereira M., Pinto L.S.R.C., Pinto L.P., Porto J.I.R., Petrich D.P.,			
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondonelli E.,			
RA Santos B.B.P., Santos F.R., Schneider M.P.C., Senaues H.N.,			
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,			
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,			
RA Souza R.C., Steffens M.B.R., Steinbald M., Teixeira S.R., Urmeyni T.,			
RA Vettore A., Wassef R., Zaha A., Simpion A.J.G.,			
RA "The complete genome sequence of Chromobacterium violaceum reveals remarkable and exploitable bacterial adaptability.";			
RT Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003).			
RL DR EMBL; AE016915; AAQ59142.1; -; Genomic DNA.			
KW Complete proteome; Hypothetical protein.			
SEQUENCE 276 AA; 30415 MW; 2A0AC5C004F17573 CRC64;			
Query Match	Score 37; DB 2; Length 276;		
Best Local Similarity	100.0%; Pred. No. 85;		
Matches	6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		

Query Match 72.5%; Score 37; DB 2; Length 276;
Best Local Similarity 100.0%; Pred. No. 85;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RT "Anopheles gambiae re-annotation.";
RL Submitted (APR 2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RG The Anopheles gambiae Sequence Committee;

RC STRAIN=PEST;

RG Anopheleinae; Anopheles.

OX NCBI_TAXID=18054;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RG "Anopheles gambiae re-annotation.";
RL Submitted (APR 2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PBST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/Genbank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAA8010859; EAA08168.1; -; Genomic_DNA.
DR InterPro; IPR011022; Arrestin_C.
DR InterPro; IPR011021; Arrestin_N.
DR Pfam; PF02752; Arrestin_C; 1.
DR Pfam; PF00333; Arrestin_N; 1.
DR SEQUENCE 341 AA; 38842 MW; 8C8EDDAE6802AA74E CRC64;
Query Match 72.5%; Score 37; DB 2; Length 341;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YFPQOF 6
Db 1.9 YFPQOF 24

Search completed: December 2, 2005, 05:57:23
Job time : 238 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

protein - protein search, using sw model

on: December 2, 2005, 05:31:45 ; Search time 187 Seconds
(without alignments)
21.147 Million cell updates/sec

title: US-10-603-566A-61

perfect score: 51 YFPQQFAFS 9

oring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

table: 2441163 seqs, 439378781 residues

arched: 2443163 hits satisfying chosen parameters:
total number of hits searched: 45

ALIGMEN 13

BT-processing: Maximum Match 0%
Listing first 45 summaries

RESULT 1
ID ADM43837 standard; peptide; 9 AA.

1: geneseqp1980s: *

2:	Genesep2>2008:	AA
3:	Genesep2>20008:*	DT
4:	Genesep2>20018:*	XX
5:	Genesep2>20028:*	DB
6:	Genesep2>20038:*	XX
7:	Genesep2>2003bs:*	KW
8:	Genesep2>20048:*	KW
9:	Genesep2>2005B:*	KW

SYNTHETIC POLYMERS

No.	Score	Match	Length	DB	ID	Description
1	51	100..0	9	9	ADW43837	Human che
2	51	100..0	9	9	ADW43915	ChemerinR
3	51	100..0	10	9	ADW43838	Human che
4	51	100..0	10	9	ADW43914	ChemerinR
5	51	100..0	11	9	ADW43861	Human che
6	51	100..0	11	9	ADW43913	ChemerinR
7	51	100..0	12	9	ADW43839	Human che
8	51	100..0	12	9	ADW43912	ChemerinR
9	51	100..0	13	9	ADW43911	ChemerinR
10	51	100..0	13	9	ADW43840	Human che
11	51	100..0	14	9	ADW43910	ChemerinR
12	51	100..0	15	9	ADW43909	ChemerinR
13	51	100..0	15	9	ADW43860	Human che
14	51	100..0	16	9	ADW43908	ChemerinR
15	51	100..0	17	9	ADW43907	ChemerinR
16	51	100..0	17	9	ADW43859	Human che
17	51	100..0	18	9	ADW43906	ChemerinR
18	51	100..0	18	9	ADX56680	Cardiovase
19	51	100..0	18	9	ADY38103	Ruman Cpp
20	51	100..0	19	9	ADW43829	Human che
21	51	100..0	19	9	ADW43798	Human che
22	51	100..0	19	9	ADW43905	ChemerinR
23	51	100..0	20	9	ADW43830	Human che
					NDW43900	
					NDW43901	
					ADW43830	
					ADW43902	
					ADW43903	
					ADW43904	
					ADW43905	
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					ADW44065	
</td						

PN WO2005000875-A2.

XX BDN 06-711N-200E

XX	PF	25-JUN-2004 ; 2004WO-EP006945.
XX	PR	25-JUN-2003 ; 2003US-00603566.
XX	PA	(EURO-) EUROSCREEN SA.
XX	PI	Wittamer V, Communi D, Deth
XX	PI	Ooms EUR;
XX	DR	WP1 ; 2005-050121/06.
XX		

e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's Disease, or histiocytosis.

PD 06-JAN-2005.
 XX
 PF 25-JUN-2004; 2004WO-EP006945.
 XX
 PR 25-JUN-2003; 2003US-00603566.
 XX
 PA (EURO-) EUROSCREEN SA.
 XX
 PI Wittamer V, Communi D, Dethieux M, Parmentier M, Loison C;
 Ooms FDR;
 DR XX
 WPI; 2005-058121/06.
 XX
 PT New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, Paraproteinemia, Purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, or histiocytosis.
 XX
 PS Example 15; SEQ ID NO 62; 183pp; English.
 XX
 CC The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also comprising the coding sequence encoding (I); an expression vector transfected with the expression vector; a (therapeutic) composition comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (I); an antibody that selectively binds to (I); identifying an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a ChemerinR polypeptide and a sample; identifying an agent that modulates the function of ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signaling; a kit, for screening agents that modulate the signaling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide signaling, comprising an isolated ChemerinR polypeptide, (I), an isolated polynucleotide encoding (I), a cell transformed with a polynucleotide encoding (I), and its packaging materials; a non-human mammal transgenic for a ChemerinR activation encoding (I); identifying an antibody inhibiting ChemerinR activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a human proChemerin peptide used to analyse processing of immature chemerin.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPQGAFAS 9
 2 YFPQGAFAS 10

RESULT 4
 ADM43914 standard; peptide; 10 AA.
 ID ADM43914;
 AC XX
 DT 24-MAR-2005 (first entry)

DB XX
 KW gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasia; cardiovascular-disen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW ChemerinR;
 XX
 OS Unidentified.
 XX
 PN WO2005000875-A2.
 XX
 PD 06-JAN-2005.
 XX
 PI Wittamer V, Communi D, Dethieux M, Parmentier M, Loison C;
 Ooms FDR;
 XX
 WPI; 2004WO-EPP006945.
 XX
 PR 25-JUN-2004; 2004WO-EPP006945.
 XX
 PR 25-JUN-2003; 2003US-00603566.
 XX
 PA (EURO-) EUROSCREEN SA.
 XX
 CC The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also comprising are: a nucleic acid sequence encoding (I); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal transfected with the expression vector; a (therapeutic) composition comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (I); an antibody that selectively binds to (I); identifying an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a ChemerinR polypeptide and a sample; identifying an agent that modulates the function of ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide; detecting the interaction between a ChemerinR polypeptide and an isolated ChemerinR polypeptide or a nucleic acid sequence of (I); an antibody that selectively binds to (I); identifying an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a ChemerinR polypeptide and a sample; identifying an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide; diagnosing an isolated ChemerinR polypeptide, (I), an isolated polynucleotide encoding (I), and its packaging materials; a non-human mammal transgenic for a ChemerinR polynucleotide encoding (I); identifying an antibody inhibiting ChemerinR and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a human proChemerin peptide used to analyse processing of immature chemerin.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPQGAFAS 9
 2 YFPQGAFAS 10

RESULT 4
 ADM43914 standard; peptide; 10 AA.
 ID ADM43914;
 AC XX
 DT 24-MAR-2005 (first entry)

DB XX
 KW gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasia; cardiovascular-disen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW ChemerinR;
 XX
 OS Unidentified.
 XX
 PN WO2005000875-A2.
 XX
 PD 06-JAN-2005.
 XX
 PI Wittamer V, Communi D, Dethieux M, Parmentier M, Loison C;
 Ooms FDR;
 XX
 WPI; 2004WO-EPP006945.
 XX
 PR 25-JUN-2004; 2004WO-EPP006945.
 XX
 PR 25-JUN-2003; 2003US-00603566.
 XX
 PA (EURO-) EUROSCREEN SA.
 XX
 CC The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also comprising are: a nucleic acid sequence encoding (I); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal transfected with the expression vector; a (therapeutic) composition comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (I); an antibody that selectively binds to (I); identifying an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a ChemerinR polypeptide and a sample; identifying an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide; diagnosing an isolated ChemerinR polypeptide, (I), an isolated polynucleotide encoding (I), and its packaging materials; a non-human mammal transgenic for a ChemerinR polynucleotide encoding (I); identifying an antibody inhibiting ChemerinR and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a human proChemerin peptide used to analyse processing of immature chemerin.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0073;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFPQGAFAS 9
 2 YFPQGAFAS 10

RESULT 4
 ADM43914 standard; peptide; 10 AA.
 ID ADM43914;
 AC XX
 DT 24-MAR-2005 (first entry)

DB XX
 KW gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;
 KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasia; cardiovascular-disen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW ChemerinR;
 XX
 OS Unidentified.
 XX
 PN WO2005000875-A2.
 XX
 PD 06-JAN-2005.
 XX
 PI Wittamer V, Communi D, Dethieux M, Parmentier M, Loison C;
 Ooms FDR;
 XX
 WPI; 2004WO-EPP006945.
 XX
 PR 25-JUN-2004; 2004WO-EPP006945.
 XX
 PR 25-JUN-2003; 2003US-00603566.
 XX
 PA (EURO-) EUROSCREEN SA.
 XX
 CC The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also comprising are: a nucleic acid sequence encoding (I); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal transfected with the expression vector; a (therapeutic) composition comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (I); an antibody that selectively binds to (I); identifying an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a ChemerinR polypeptide and a sample; identifying an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide; diagnosing an isolated ChemerinR polypeptide, (I), an isolated polynucleotide encoding (I), and its packaging materials; a non-human mammal transgenic for a ChemerinR polynucleotide encoding (I); identifying an antibody inhibiting ChemerinR and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a human proChemerin peptide used to analyse processing of immature chemerin.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 51; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0073;

sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signaling; a kit, for screening agents that modulate the signaling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide signaling, comprising an isolated ChemerinR polypeptide, (1), an isolated polynucleotide encoding (1), a cell transformed with a polynucleotide encoding (1), and its packaging materials; a non-human mammal transgenic for a ChemerinR polynucleotide encoding (1); identifying an antibody inhibiting Chemerin activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemias, purpura, sarcoidosis, Sezary's Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a polypeptide associated with activation of the human chemerin receptor (chemerinR).

Sequence 11 AA;

Query Match Score 51; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.008; Gaps 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9
1 ||||| |||
Db 3 YFPQQFAFS 11

RESULT 7

ADW43839 standard; peptide; 12 AA.
ID ADW43839
AC ADW43839;

XX 24-MAR-2005 (first entry)

DE Human chemerin peptide SEQ ID NO 63.

KW gene therapy; diagnosis; cell signaling; gene therapy;
KW lymphoproliferative disease; dermatological disease; dermatological;
KW hemostatic; inflammation; antiinflammatory; hematological disease;
KW immune disorder; neoplasm; cardiovascular-gen; CNS-gen;
KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.
XX Homo sapiens.

XX WO200500875-A2.

XX 06-JAN-2005.

PF 25-JUN-2004; 2004WO-EP006945.

PR 25-JUN-2003; 2003US-00603566.

XX (EURO-) EUROSCREEN SA.

PI Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;

PI Ooms FDR;

XX DR 2005-058121/06.

XX New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, or histiocytosis.

XX Example 15; SEQ ID NO 63; 163pp; English.

XX The invention describes a polypeptide (1) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also described are: a nucleic acid sequence encoding (1); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal comprising (1) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (1); an antibody that selectively binds to (1); identifying an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide in a sample; identifying an agent that modulates the function of ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signaling; a kit, for screening agents that modulate the signaling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide signaling, comprising an isolated ChemerinR polypeptide, (1), an isolated polynucleotide encoding (1), a cell transformed with a polynucleotide encoding (1), and its packaging materials; a non-human mammal transgenic for a ChemerinR polynucleotide encoding (1); identifying an antibody inhibiting Chemerin activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a human prochemerin peptide used to analyse processing of immature chemerin.

XX Sequence 12 AA;

XX SQ

Query Match Score 51; DB 9; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.008; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9
1 ||||| |||
Db 4 YFPQQFAFS 12

RESULT 8

ADW43912
ID ADW43912 standard; peptide; 12 AA.
XX AC ADW43912;

XX DT 24-MAR-2005 (first entry)

XX DB ChemerinR activation associated polypeptide #39.

XX KW gene therapy; diagnosis; cell signaling; gene therapy;
KW lymphoproliferative disease; dermatological disease; dermatological;
KW hemostatic; inflammation; antiinflammatory; hematological disease;
KW immune disorder; neoplasm; cardiovascular-gen; CNS-gen;
KW neurological disease; hyperproliferative disorders; cytostatic;
KW chemerinR.
XX Unidentified.

XX OS WO200500875-A2.

XX DT 06-JAN-2005.

XX DB ChemerinR activation associated polypeptide #39.

XX KW gene therapy; diagnosis; cell signaling; gene therapy;

KW lymphoproliferative disease; dermatological disease; dermatological;

KW hemostatic; inflammation; antiinflammatory; hematological disease;

KW immune disorder; neoplasm; cardiovascular-gen; CNS-gen;

KW neurological disease; hyperproliferative disorders; cytostatic;

XX PD 06-JAN-2005.

XX PR 25-JUN-2004; 2004WO-EP006945.

XX PR 25-JUN-2003; 2003US-00603566.

PS

XX (EURO-) EUROSCREEN SA.
 XX Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;
 PI Ooms FDR;
 XX DR WPI; 2005-058121/06.
 XX New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemas, purpura, sarcoidosis, Seary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, or histiocytosis
 XX Disclosure: Page 105; 183pp; English.
 XX The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also comprising are: a nucleic acid sequence encoding (I); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal transfected with the expression vector; a (therapeutic) composition comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (I); an antibody that selectively binds to (I); identifying an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide in a sample; identifying an agent that modulates the function of ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signaling; a kit, for screening agents that modulate the signaling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide, comprising an isolated ChemerinR polypeptide, (I), an isolated polynucleotide encoding (I), a cell transformed with a polynucleotide encoding (I), and its packaging materials; a non-human mammal transgenic for a ChemerinR polynucleotide encoding (I); identifying an antibody inhibiting ChemerinR activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemas, purpura, sarcoidosis, Seary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a polypeptide associated with activation of the human chemerin receptor (ChemerinR).
 XX Sequence 12 AA:
 XX Query Match 100.0%; Score 51; DB 9; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.0081;
 Matches 9; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;
 XX Qy 1 YFPGQPAFS 9
 DB 4 YPPGQPAFS 12
 XX RESULT 9
 ID ADW43911 standard; peptide; 13 AA.
 XX ADW43911;
 XX AC ADW43911;
 XX DT 24-MAR-2005 (first entry)
 XX DB ChemerinR activation associated polypeptide #38.
 XX KW gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological

KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular disease; CNS-Gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW chemerinR.
 XX OS Unidentified.
 XX PN WO2005000875-A2.
 XX 06-JAN-2005.
 XX 25-JUN-2004; 2004WO-EPP006945.
 XX 25-JUN-2003; 2003US-00603566.
 XX (EURO-) EUROSCREEN SA.
 XX PA
 XX PI Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;
 PI Ooms FDR;
 XX WPI; 2005-058121/06.
 XX New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemas, purpura, sarcoidosis, Seary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, or histiocytosis.
 XX Disclosure; Page 105; 183pp; English.
 XX The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also comprising are: a nucleic acid sequence encoding (I); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal transfected with the expression vector; a (therapeutic) composition comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (I); an antibody that selectively binds to (I); identifying an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide in a sample; identifying an agent that modulates the function of ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signaling; a kit, for screening agents that modulate the signaling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide signaling, comprising an isolated ChemerinR polypeptide, (I), an isolated polynucleotide encoding (I), a cell transformed with a polynucleotide encoding (I), and its packaging materials; a non-human mammal transgenic for a ChemerinR polynucleotide encoding (I); identifying an antibody inhibiting ChemerinR activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemas, purpura, sarcoidosis, Seary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a polypeptide associated with activation of the human chemerin receptor (ChemerinR).
 XX Sequence 13 AA:
 XX Query Match 100.0%; Score 51; DB 9; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0095;
 Matches 9; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;
 XX Qy 1 YFPGQPAFS 9
 DB 5 YPPGQPAFS 13

RESULT 10
 ADW43840 standard; peptide; 13 AA.
 XX
 AC ADW43840;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Human chemerin peptide SEQ ID NO 64.
 XX
 KW gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease;
 KW hematocrit; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.
 XX
 OS Homo sapiens.
 PN WO2005000875-A2.
 XX
 PD 06-JAN-2005.
 XX
 PF 25-JUN-2004; 2004WO-EP006945.
 XX
 PR 25-JUN-2003; 2003US-00603566.
 XX
 (EURO-) EUROSCREEN SA.
 XX
 PA Wittamer V, Communi D, Dethieux M, Parmentier M, Loison C;
 PI Ooms FDR;
 XX
 DR WPI; 2005-058121/06.
 XX
 PT New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, Purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, or histiocytosis.
 XX
 PS Example 15; SEQ ID NO 64; 183pp; English.
 XX
 CC The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a Chemerin polypeptide. Also described are: a nucleic acid sequence encoding (I); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (I); an antibody that selectively binds to (I); identifying an agent that modulates the interaction between a Chemerin polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a Chemerin polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signaling a kit, for screening agents that modulate the signaling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide signaling, comprising an isolated ChemerinR polypeptide, (I), an isolated polynucleotide encoding (I), a cell transformed with a polynucleotide encoding (I), and its packaging materials; a non-human mammal transgenic for a Chemerin polynucleotide encoding (I); identifying an antibody inhibiting ChemerinR activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemias, Purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a human prochemerin peptide used to analyse processing of immature Chemerin.

XX
 Sequence 13 AA;

Query Match 100.0%; Score 51; DB 9; Length 13;
 Best Local Similarity 100.0%; Prd. No. 0.0095;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9
 |||||
 Db 5 YFPQQFAFS 13

RESULT 11
 ID ADW43910 standard; peptide; 14 AA.
 XX
 AC ADW43910;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE ChemerinR activation associated polypeptide #37.
 XX
 KW gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological disease;
 KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW chemerinR.
 XX
 OS Unidentified.
 XX
 PN WO2005000875-A2.
 XX
 PD 06-JAN-2005.
 XX
 PF 25-JUN-2004; 2004WO-EP006945.
 XX
 PR 25-JUN-2003; 2003US-00603566.
 XX
 (EURO-) EUROSCREEN SA.

PI Wittamer V, Communi D, Dethieux M, Parmentier M, Loison C;
 PI Ooms FDR;
 XX
 DR WPI; 2005-058121/06.

PT New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, Purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, or histiocytosis.
 XX
 PS Disclosure; Page 105; 183pp; English.

CC The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also described are: a nucleic acid sequence encoding (I); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (I); an antibody that selectively binds to (I); identifying an agent that modulates the interaction between a Chemerin polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a Chemerin polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signaling a kit, for screening agents that modulate the signaling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide signaling, comprising an isolated ChemerinR polypeptide, (I), an isolated polynucleotide encoding (I), a cell transformed with a polynucleotide encoding (I), and its packaging materials; a non-human mammal transgenic for a Chemerin polynucleotide encoding (I); identifying an antibody inhibiting ChemerinR activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemias, Purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a human prochemerin peptide used to analyse processing of immature Chemerin.

XX
 Sequence 13 AA;

Query Match 100.0%; Score 51; DB 9; Length 13;
 Best Local Similarity 100.0%; Prd. No. 0.0095;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPQQFAFS 9
 |||||
 Db 5 YFPQQFAFS 13

RESULT 12
 ID ADW43910 standard; peptide; 14 AA.
 XX
 AC ADW43910;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE ChemerinR activation associated polypeptide #37.
 XX
 KW gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological disease;
 KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW chemerinR.
 XX
 OS Unidentified.
 XX
 PN WO2005000875-A2.
 XX
 PD 06-JAN-2005.
 XX
 PF 25-JUN-2004; 2004WO-EP006945.
 XX
 PR 25-JUN-2003; 2003US-00603566.
 XX
 (EURO-) EUROSCREEN SA.

PI Wittamer V, Communi D, Dethieux M, Parmentier M, Loison C;
 PI Ooms FDR;
 XX
 DR WPI; 2005-058121/06.

PT New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, Purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, or histiocytosis.
 XX
 PS Disclosure; Page 105; 183pp; English.

CC The invention describes a polypeptide (I) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also described are: a nucleic acid sequence encoding (I); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (I); an antibody that selectively binds to (I); identifying an agent that modulates the interaction between a Chemerin polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a Chemerin polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signaling a kit, for screening agents that modulate the signaling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide signaling, comprising an isolated ChemerinR polypeptide, (I), an isolated polynucleotide encoding (I), a cell transformed with a polynucleotide encoding (I), and its packaging materials; a non-human mammal transgenic for a Chemerin polynucleotide encoding (I); identifying an antibody inhibiting ChemerinR activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemias, Purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a human prochemerin peptide used to analyse processing of immature Chemerin.

ChemerinR polypeptide signaling, comprising an isolated ChemerinR polypeptide, (1), an isolated polynucleotide encoding (1), a cell transformed with a polynucleotide encoding for a ChemerinR polynucleotide materials; a non-human mammal transgenic for a ChemerinR activation; encoding (1); identifying an antibody inhibiting ChemerinR activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemia, purpura, sarcoidosis, Sjögren Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a polypeptide associated with activation of the human chemerin receptor (ChemerinR).

Sequence 14 AA:

Query Match 100.0%; Score 51; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YFPQGQFAPS 9
Db 6 YFPQGQFAPS 14

RESULT 12

ADW433909 standard; peptide; 15 AA.
ID ADW433909;
XX AC ADW433909;

XX DT 24-MAR-2005 (first entry)

DE ChemerinR activation associated polypeptide #336.
XX Gene therapy; diagnosis; cell signaling; gene therapy;
KW lymphoproliferative disease; dermatological disease; hematological disease;
KW hemorrhatic; inflammation; antinflammatory; hemato-
immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
KW neurological disease; hyperproliferative disorders; cytostatic;
KW chemerinR.

XX Unidentified.

OS XX

PN WO2005000875-A2.

XX PD 06-JAN-2005.

XX 25-JUN-2004; 2004WO-EP006945.

XX 25-JUN-2003; 2003US-00603566.

XX (EURO-) EUROSCREEN SA.

XX Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;

PI PI Ooms FDR;

XX DR WPI; 2005-058121/06.

XX New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura, sarcoidosis, Sjögren Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, or histiocytosis.

XX Disclosure; Page 104; 183pp; English.

XX The invention describes a polypeptide (1) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also described are: a nucleic acid sequence encoding (1); an expression vector

comprising the coding sequence of the nucleic acid; a transgenic animal transfected with the expression vector; a (therapeutic) composition comprising (1) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (1); an antibody that selectively binds to (1); identifying an agent that modulates the interaction between a ChemerinR polypeptide and ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide in a sample; identifying an agent that modulates the function of ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signaling; a kit, for screening agents that modulate the signaling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide signaling, comprising an isolated ChemerinR polypeptide, (1), an isolated polynucleotide encoding (1), a cell transformed with a polynucleotide encoding for a ChemerinR polynucleotide materials; a non-human mammal transgenic for a ChemerinR polynucleotide encoding (1); identifying an antibody inhibiting ChemerinR activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemia, purpura, sarcoidosis, Sjögren Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a polypeptide associated with activation of the human Chemerin receptor (ChemerinR).

Sequence 15 AA:

Query Match 100.0%; Score 51; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0; N mismatches 0; Del 0; Gaps 0;

Qy 1 YFPQGQFAPS 9
Db 7 YFPQGQFAPS 15

RESULT 13
ADW43860

ID ADW43860 standard; peptide; 15 AA.
XX AC ADW43860;
XX DT 24-MAR-2005 (First entry)

DE Human Chemerin peptide SEQ ID NO 84.
XX Gene therapy; diagnosis; cell signaling; gene therapy;
KW lymphoproliferative disease; dermatological disease; hematological disease;
KW hemorrhatic; inflammation; antinflammatory; hemato-
immune disorder; neoplasm; cardiovascular-gen.; cns-gen.;
KW neurological disease; hyperproliferative disorders; cytostatic;
KW chemerinR.
XX Homo sapiens.
XX WO2005000875-A2.

XX 06-JAN-2005.
XX 25-JUN-2004; 2004WO-EP006945.
XX 25-JUN-2003; 2003US-00603566.
XX (EURO-) EUROSCEEN SA.
XX Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;
PI PI Ooms FDR;
XX DR WPI; 2005-058121/06.

XX The invention describes a polypeptide (1) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also described are: a nucleic acid sequence encoding (1); an expression vector

XX WPI; 2005-058121/06.
 XX
 PT New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, or histiocytosis.
 XX Disclosure: SEQ ID NO 84; 183pp; English.
 XX The invention describes a polypeptide (1) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also described are: a nucleic acid sequence encoding (1); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal transfected with the expression vector; a (therapeutic) composition comprising (1) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (1), that selectively binds to (1); identifying an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide in a sample; identifying an agent that modulates the function of ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signalling; a kit, for screening agents that modulate the signalling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide signalling, comprising an isolated ChemerinR polypeptide, (1), an isolated polynucleotide encoding (1), a cell transformed with an isolated polynucleotide encoding (1), and its packaging materials; a non-human mammal transgenic for a ChemerinR polynucleotide encoding (1); identifying an antibody inhibiting ChemerinR activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a human proChemerin peptide used to analyse processing of immature chemerin.
 XX Sequence 15 AA;
 Query Match 100.0%; Score 51; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Gaps 0;
 Matches 9; Conservative 0; Indels 0;
 Qy 1 YFPQQPQAFS 9
 Db 7 YFPQQPQAFS 15

RESULT 14
 ID ADW43908
 XX ADW43908 standard; peptide; 16 AA.
 AC ADW43908;
 DT 24-MAR-2005 (first entry)
 XX ChemerinR activation associated polypeptide #35.
 XX Gene therapy; diagnosis; cell signaling; gene therapy;
 KW Lymphoproliferative disease; dermatological disease; dermatological
 KW hemostatic; inflammation; antinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; CNS-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic;
 KW chemerinR.
 XX

OS Unidentified.
 XX
 PN WO2005008875-A2.
 XX
 PT 06-JAN-2005.
 XX
 PT 25-JUN-2004; 2004WO-EP006945.
 XX
 PR 25-JUN-2003; 2003US-00603566.
 XX
 PA (EURO-) EUROSCREEN SA.
 XX
 PT New Chemerin polypeptides, useful for diagnosing and treating a disease, e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, or histiocytosis.
 XX
 DR WPI; 2005-058121/06.
 XX
 PS Disclosure; Page 104; 183pp; English.
 XX
 CC The invention describes a polypeptide (1) of up to 50 amino acids where the polypeptide binds specifically to a ChemerinR polypeptide. Also described are: a nucleic acid sequence encoding (1); an expression vector comprising the coding sequence of the nucleic acid; a transgenic animal transfected with the expression vector; a (therapeutic) composition comprising (1) and an isolated ChemerinR polypeptide or a nucleic acid sequence of (1); an antibody that selectively binds to (1); identifying an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the interaction between a ChemerinR polypeptide and a ChemerinR polypeptide; identifying an agent that modulates the function of ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR (polypeptide) signalling, a kit, for screening agents that modulate the signalling activity of ChemerinR polypeptide or for diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide; identifying an agent that modulates the function of ChemerinR polypeptide; detecting the presence, in a sample, of an agent that modulates the function of ChemerinR polypeptide; diagnosing a disease or disorder characterized by dysregulation of ChemerinR polypeptide; identifying an isolated polynucleotide encoding (1), a cell transformed with a polynucleotide encoding (1), and its packaging materials; a non-human mammal transgenic for a ChemerinR polynucleotide encoding (1); identifying an antibody inhibiting ChemerinR activation; and an in vitro method of inhibiting cell proliferation. The (therapeutic) composition or expression vector is useful for preparing a medicament for ex vivo gene therapy or for in vivo gene therapy or a medicament for inhibiting cell proliferation, where the medicament is used for treating a disease, e.g. neoplasms, hypergammaglobulinemia, lymphoproliferative diseases, disorders, and/or conditions, paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease. The polypeptides and polynucleotides and methods are useful for diagnosing and treating the cited diseases. This is the amino acid sequence of a polypeptide associated with activation of the human chemerin receptor (ChemerinR).
 XX Sequence 16 AA;
 SQ Query Match 100.0%; Score 51; DB 9; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.012; Mismatches 0; Indels 0; Gaps 0;
 Matches 9; Conservative 0;
 Qy 1 YFPQQPQAFS 9
 Db 8 YFPQQPQAFS 16

RESULT 15
 ID ADW43907
 ADW43907 standard; peptide; 17 AA.
 XX

XX ADW43907;
 XX DT 24-MAR-2005 (first entry)
 XX ChemerinR activation associated polypeptide #24.
 XX gene therapy; diagnosis; cell signaling; gene therapy;
 XX lymphoproliferative disease; dermatological disease; dermatological
 XX hemostatic; inflammation; antiinflammatory; hematological disease;
 XX immune disorder; neoplasm; cardiovascular gen.; CNS-gen.;
 XX neurologic disease; hyperproliferative disorders; cytostatic;
 XX ChemerinR.
 XX Unidentified.
 XX WO2005000875-A2.
 XX PN 06-JAN-2005.
 XX PP 25-JUN-2004; 2004WO-EP006945.
 XX PR 25-JUN-2003; 2003US-00603566.
 XX PA (EURO-) EUROSCREEN SA.
 XX Wittamer V, Communi D, Detheux M, Parmentier M, Loison C;
 PI Ooms FDR;
 XX DR; 2005-058121/06.
 XX PT New Chemerin polypeptides, useful for diagnosing and treating a disease,
 PR e.g. neoplasms, hypergammaglobulinemia, paraproteinemia, purpura,
 PR sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's
 PR Disease, or histiocytosis.
 XX Disclosure; Page 104; 183pp; English.
 XX The invention describes a polypeptide (I) of up to 50 amino acids where
 CC the polypeptide binds specifically to a ChemerinR polypeptide. Also
 CC described are: a nucleic acid sequence encoding (I); an expression vector
 CC comprising the coding sequence of the nucleic acid; a transgenic animal
 CC transfected with the expression vector; a (therapeutic) composition
 comprising (I) and an isolated ChemerinR polypeptide or a nucleic acid
 CC sequence of (I); an antibody that selectively binds to (I); identifying
 CC an agent that modulates the interaction between a Chemerin polypeptide
 CC and a ChemerinR polypeptide; detecting the presence, in a sample, of an
 CC agent that modulates the interaction between a Chemerin polypeptide and a
 CC ChemerinR polypeptide in a sample; identifying an agent that modulates
 CC the function of ChemerinR polypeptide; detecting the presence, in a
 CC sample, of an agent that modulates the function of ChemerinR polypeptide;
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC ChemerinR (polypeptide) signaling; a kit, for screening agents that
 CC modulate the signaling activity of ChemerinR polypeptide or for
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC ChemerinR polypeptide signaling, comprising an isolated ChemerinR
 CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell
 CC transformed with a polynucleotide encoding (I), and its packaging
 CC materials; a non-human mammal transgenic for a ChemerinR polynucleotide
 CC encoding (I); identifying an antibody inhibiting ChemerinR activation;
 CC and an in vitro method of inhibiting cell proliferation. The
 CC (therapeutic) composition or expression vector is useful for preparing a
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
 CC medicament for inhibiting cell proliferation, where the medicament is
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
 CC lymphoproliferative diseases, disorders, and/or conditions,
 CC paraproteinemia, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's
 CC Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other
 CC hyperproliferative disease. The polypeptides and polynucleotides and
 CC methods are useful for diagnosing and treating the cited diseases. This
 CC is the amino acid sequence of a polypeptide associated with activation of
 CC the human Chemerin receptor (ChemerinR).

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November 2005

Published_Applications_Nucleic Acid and Published_Applications_Amino Acid databases now generate two sets of results each. The Published_Applications_Amino Acid database searches now reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results with the extensions .rnpbm (Published_Applications_NA_Main) and .rnppn (Published_Applications_NA_New). Searches run against Amino Acid Published_Applications produce two sets of results with the extensions .rapbm (Published_Applications_AA_Main) and .rapbn (Published_Applications_AA_New).

GenCore version 5.1.6
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protein - protein search, using sw model

on: December 2, 2005, 05:52:46 ; Search time 11 Seconds
 (without alignments)
 3.918 Million cell updates/sec

title: US-10-603-566A-61

perfect score: 51

Sequence: 1 YFFGQAFS 9

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 26661 seqs, 4788334 residues

total number of hits satisfying chosen parameters: 26661

minimum DB seq length: 0

maximum DB seq length: 2000000000

st-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 4 summaries

database : Published Applications AA_New:*

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2: /cgn_6/produca_1/pubpaas/US06_NEW_PUB_pep:*

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4: /cgn_6/produca_1/pubpaas/US08_NEW_PUB_pep:*

5: /cgn_6/produca_1/pubpaas/PCT_NEW_PUB_pep:*

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7: /cgn_6/produca_1/pubpaas/US11_NEW_PUB_pep:*

8: /cgn_6/produca_1/pubpaas/US12_NEW_PUB_pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	NCBI	Score	Query	Match	Length	DB	ID	Description
1	37	72.5	532	6	US-10-821-234-918	Sequence 918, App	Sequence 918, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
2	32	62.7	116	7	US-11-174-186-18	Sequence 18, App	Sequence 18, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
3	32	62.7	117	7	US-11-174-186-35	Sequence 35, App	Sequence 35, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
4	32	62.7	259	6	US-10-512-184-31	Sequence 31, App	Sequence 31, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
5	32	62.7	259	6	US-10-512-184-33	Sequence 33, App	Sequence 33, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
6	32	62.7	329	6	US-10-512-184-68	Sequence 68, App	Sequence 68, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
7	32	62.7	329	6	US-10-512-184-70	Sequence 70, App	Sequence 70, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
8	32	62.7	397	6	US-10-467-637-4202	Sequence 4202, App	Sequence 4202, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
9	32	62.7	537	6	US-11-174-186-41	Sequence 4136, App	Sequence 4136, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
10	31	60.8	301	6	US-10-467-637-1620	Sequence 1620, App	Sequence 1620, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
11	31	60.8	372	6	US-10-793-626A-166	Sequence 166, App	Sequence 166, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
12	31	59.8	116	7	US-11-174-186-41	Sequence 41, App	Sequence 41, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
13	30	59.8	754	6	US-10-467-637-4202	Sequence 1620, App	Sequence 1620, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
14	30	59.8	116	7	US-11-174-186-41	Sequence 63, App	Sequence 63, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
15	29	56.9	117	7	US-11-174-186-25	Sequence 25, App	Sequence 25, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
16	29	56.9	185	6	US-10-467-557-9059	Sequence 9059, App	Sequence 9059, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
17	29	56.9	185	6	US-10-467-657-1228	Sequence 1228, App	Sequence 1228, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
18	29	56.9	564	7	US-11-084-554-58	Sequence 78, App	Sequence 78, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
19	29	56.9	1627	6	US-10-821-234-1283	Sequence 1283, App	Sequence 1283, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
20	28	54.9	21	6	US-10-339-830-609	Sequence 609, App	Sequence 609, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
21	28	54.9	60	7	US-11-091-668-8	Sequence 8, App	Sequence 8, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
22	28	54.9	98	7	US-11-054-669-47	Sequence 47, App	Sequence 47, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
23	28	54.9	98	7	US-11-084-554-58	Sequence 58, App	Sequence 58, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
24	28	54.9	116	7	US-11-174-186-2	Sequence 26, App	Sequence 26, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0
25	28	54.9	116	7	US-11-174-186-26	Sequence 26, App	Sequence 26, App	Query Match 72.5%; Best Local Similarity 75.0%; Matches 6; Conservative 6; Pred. No. 3.4%; Mismatches 0; Indels 0; Gaps 0

RESULTS

RESULT 1
 US-10-821-234-918
 ; Sequence 918, Application US/10821234
 ; Publication No. US20050255114A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Labat, Ivan
 ; STACHE-CRAIN, Birgit
 ; ADDRESS: Andarmani, Susan
 ; TANG, Y. Tom
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 ; FILE REFERENCE: 821A
 ; CURRENT APPLICATION NUMBER: US/10/821, 234
 ; CURRENT FILING DATE: 2004-04-07
 ; PRIOR APPLICATION NUMBER: US 60/462, 047
 ; PRIOR FILING DATE: 2003-04-07
 ; NUMBER OF SEQ ID NOS: 1704
 ; SOFTWARE: pt_SEQ_Genes Version 1.0
 ; SEQ ID NO: 918
 ; LENGTH: 532
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-821-234-918

RESULT 2
 US-11-174-186-18
 ; Sequence 18, Application US/11174186
 ; Publication No. US2005024418A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gillies, Stephen
 ; ADDRESS: Lo, Kin-Ming
 ; TANG, Xiang
 ; TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
 ; FILE REFERENCE: LEX-019
 ; CURRENT APPLICATION NUMBER: US/11/174, 186
 ; CURRENT FILING DATE: 2005-07-01
 ; PRIOR APPLICATION NUMBER: US 60/288, 564
 ; PRIOR FILING DATE: 2001-05-03
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: Parental version 3.3

```

; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: VH7 heavy chain
US-11-174-186-18

Query Match
Best Local Similarity 62.7%; Score 32; DB 7; Length 116;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
RESULT 3
US-11-174-186-35
Sequence 35, Application US/11174186
Publication No. US20050244190A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xiugu
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35
LENGTH: 117
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: VH369 heavy chain
US-11-174-186-35

Query Match
Best Local Similarity 62.7%; Score 32; DB 7; Length 117;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
RESULT 4
US-10-512-184-31
Sequence 31, Application US/10512184
Publication No. US2005024490A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: antibody fragments and fusions against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 259
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: scFv VDcw with
OTHER INFORMATION: specificity against Vorticillium dahliae;
OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-31

Query Match
Best Local Similarity 62.7%; Score 32; DB 6; Length 259;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
RESULT 5
US-10-512-184-33
Sequence 33, Application US/10512184
Publication No. US2005024490A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi.
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 33
LENGTH: 259
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: scFv PL2 with
OTHER INFORMATION: specificity against Phoma lingam; originates from
OTHER INFORMATION: Mus musculus.
US-10-512-184-33

Query Match
Best Local Similarity 62.7%; Score 32; DB 6; Length 259;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
RESULT 6
US-10-512-184-68
Sequence 68, Application US/10512184
Publication No. US2005024490A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: resistance against fungi.
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 68
LENGTH: 329
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: precursor
OTHER INFORMATION: fusion protein comprising RS - linker scFv VD2.
US-10-512-184-68

Query Match
Best Local Similarity 62.7%; Score 32; DB 6; Length 329;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
RESULT 7
US-10-512-184-68
Sequence 68, Application US/10512184
Publication No. US2005024490A1
GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies, recombinant antibodies, recombinant antibody fragments and fusions mediated plant disease
TITLE OF INVENTION: antibody fragments and fusions against fungi
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 31
LENGTH: 259
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: scFv VDcw with
OTHER INFORMATION: specificity against Vorticillium dahliae;
OTHER INFORMATION: originates from Mus musculus.
US-10-512-184-31

```

RESULT 7 US-10-512-184-70
Sequence 70, Application US/10512184
 GENERAL INFORMATION:
APPLICANT: Fraunhofer Gesellschaft zur Förderung der angewandten Forschung e.V.
TITLE OF INVENTION: Antibodies recombinant antibodies recombinant
TITLE OF INVENTION: antibody fragments and fusions mediated plant disease
FILE REFERENCE: 3581.01US01
CURRENT APPLICATION NUMBER: US/10/512,184
CURRENT FILING DATE: 2004-10-22
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 70
LENGTH: 329
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Precursor
OTHER INFORMATION: fusion protein comprising RS - linker - scFv VDM2.
US-10-512-184-70

Query Match Best Local Similarity 62.7%; Score 32; DB 6; Length 329;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 10
US-11-174-186-41
Sequence 41, Application US/11174186
Publication No. US2005024416A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xiuli
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIOR APPLICATION NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn version 3.3
SEQ ID NO: 41
LENGTH: 579
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: heavy chain-IL2
US-11-174-186-41

Query Match Best Local Similarity 62.7%; Score 32; DB 7; Length 579;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 RESULT 11
US-10-467-657-1620
Sequence 1620, Application US/10467657
Publication No. US2005026058A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: MASNIGNANI Vega
APPLICANT: MONACI Elisabetta
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657

RESULT 8 US-10-467-657-4202
Sequence 4202, Application US/10467657
 GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASNIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO: 4202
LENGTH: 397
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4202

Query Match Best Local Similarity 62.7%; Score 32; DB 6; Length 397;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 RESULT 12
US-10-467-657-1620
Sequence 1620, Application US/10467657
Publication No. US2005026058A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: MASNIGNANI Vega
APPLICANT: MONACI Elisabetta
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657

RESULT 9 US-10-467-657-4136
Sequence 4136, Application US/10467657
 GENERAL INFORMATION:
APPLICANT: CHIRON SPA

US-10-131-826A-166
 CURRENT FILING DATE: 2003-08-11
 PRIOR APPLICATION NUMBER: GB-0103424.8
 NUMBER OF SEQ ID NOS: 9218
 SOFTWARE: SeqWin99, version 1.04
 SEQ ID NO: 1620
 LENGTH: 80
 TYPE: PRF
 ORGANISM: *Neisseria gonorrhoeae*
 US-10-467-657-1620

Query Match 60.8%; Score 31; DB 6; Length 80;
 Best Local Similarity 71.4%; Pred. No. 7.1;
 Matches 5; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 3 PGQFAFS 9
 Db 63 PGRAFAEN 69

RESULT 12
 US-10-131-826A-166
 Query Match 60.8%; Score 31; DB 6; Length 80;
 Best Local Similarity 71.4%; Pred. No. 7.1;
 Matches 5; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 3 PGQFAFS 9
 Db 63 PGRAFAEN 69

RESULT 13
 US-10-793-626-1632
 Query Match 60.8%; Score 31; DB 6; Length 301;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 5; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Qy 1 YFPGQ 5
 Db 183 YFPGQ 187

RESULT 14
 US-10-793-626-1632
 Query Match 60.8%; Score 30; DB 6; Length 372;
 Best Local Similarity 71.4%; Pred. No. 47;
 Matches 5; Conservative 1; Mismatches 1;
 Indels 0; Gaps 0;

Qy 2 FPGQFAF 8
 Db 329 YPGVFAF 335

RESULT 15
 US-10-467-962B-63
 Query Match 58.8%; Score 30; DB 6; Length 372;
 Best Local Similarity 71.4%; Pred. No. 47;
 Matches 5; Conservative 1; Mismatches 1;
 Indels 0; Gaps 0;

Qy 2 FPGQFAF 8
 Db 329 YPGVFAF 335

RESULT 16
 US-10-467-962B-63
 Query Match 58.8%; Score 30; DB 6; Length 754;
 Best Local Similarity 44.4%; Pred. No. 93;
 Matches 4; Conservative 3; Mismatches 2;
 Indels 0; Gaps 0;

Qy 1 YFPGQFAFS 9
 Db 291 YFPDQX 299

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 SEQ ID NO 166
 LENGTH: 101
 SOFTWARE: SeqWin99, version 1.04
 NUMBER OF SEQ ID NOS: 550
 SEQ ID NO: 166
 LENGTH: 101
 ORGANISM: Homo Sapien

RESULT 15
US-11-174-186-25
Sequence 25, Application US/11174186
Publication No. US20050244418A1
GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
APPLICANT: Lo, Kin-Ming
APPLICANT: Qian, Xiugui
TITLE OF INVENTION: Recombinant Tumor Specific Antibody And Use Thereof
FILE REFERENCE: LEX-019
CURRENT APPLICATION NUMBER: US/11/174,186
CURRENT FILING DATE: 2005-07-01
PRIORITY NUMBER: US 60/288,564
PRIOR FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn. version 3.3
SEQ ID NO: 25
LENGTH: 116
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: KS de-immunized VH5
US-11-174-186-25

Query Match 56.9%; Score 29; DB 7; Length 116;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FPGQAFS 9
|:|||:
Db 64 FKGPFPT 71

Search completed: December 2, 2005, 05:58:47
Job time : 12 secs

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OM protein - protein search, using sw model

Run on: December 2, 2005, 05:45:05 ; Search time 37 Seconds
23.404 Million cell updates/sec (without alignments)

Title: US-10-603-566A-61

Perfect score: 51

Sequence: 1 YFPQFQAFS 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	72.5	338	2 T10544	inositol 1,3,4-tri
2	37	72.5	509	1 A48528	membrane glycoprot
3	37	72.5	636	2 D82679	hypothetical prote
4	36	70.6	443	2 G90388	thermospine precur
5	36	70.6	489	2 S50396	hypothetical prote
6	36	70.6	909	2 S32538	cGMP-gated cation
7	36	70.6	961	2 A82270	excinuclease ABC c
8	36	70.6	970	2 S77349	excinuclease ABC c
9	36	70.6	1310	1 I53597	proline dehydrogen
10	36	70.6	1320	1 D64843	proline dehydrogen
11	36	70.6	1320	1 S66279	proline dehydrogen
12	36	70.6	1320	1 AB0633	proline dehydrogen
13	36	70.6	1320	2 D90786	proline dehydrogen
14	36	70.6	1320	2 B85646	proline dehydrogen
15	36	70.6	1320	2 AH0225	1-pyrroline-5-carb
16	35	68.6	341	1 RGOOBE	GRP binding regula
17	35	68.6	1014	2 T36031	excinuclease ABC c
18	34	66.7	248	2 S16417	homotopic protein H
19	34	66.7	281	2 A82104	conserved, hypothet
20	34	66.7	306	2 H75366	tRNA delta-2 isope
21	34	66.7	318	2 G70858	probable electron
22	34	66.7	318	2 T45397	FixB (imported) -
23	34	66.7	435	2 G86978	hypothetical prote
24	34	66.7	441	2 A70346	conserved, hypothet
25	34	66.7	499	2 T32688	hypothetical prote
26	34	66.7	662	2 H82401	conserved, hypothet
27	34	66.7	703	1 WMBET7	UL17 protein - hum
28	33	64.7	141	2 B85865	hypothetical prote
29	33	64.7	141	2 C91021	hypothetical prote

ALIGNMENTS

RESULT 1

T10544 inositol 1,3,4-trisphosphate 5/6-kinase homolog T12G13.10 - Arabidopsis thaliana

C:Species: Arabidopsis Thaliana (mouse-ear Cress)

C:Date: 16-Jul-1999 #sequence_change 09-Jul-2004

C:Accession: T10544

R:Bevan, M.; Leonard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barreil, B.G.; Ben-

Submitted to the Protein Sequence Database, June 1999

A:Reference number: 216533

A:Accession: T10544

A:Name: ATSP-T12G13.10

A:Molecule type: DNA

A:Residues: 1-338 <BEV>

A:Cross references: UNIPROT:Q9SUG3; UNIPARC:UP10000048910; EMBL:AL080252; GSPPDB:GN000.

A:Experimental source: cultivar Columbia; BAC clone T12G13

C:Genetics:

A:Gene: ATSP-T12G13.10

A:Map position: 4

A:Introns: 65/2; 92/3; 103/3; 144/1; 175/1; 215/1; 274/1; 292/3

Query Match 72.5% ; Score 37 ; DB 2 ; Length 338 ;
Best Local Similarity 75.0% ; Prod. No. 19 ;
Matches 6 ; Conservative 1 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;

QY 1 YFPQFQAF 8
Db 318 YFPQFQAF 325

RESULT 2

A8528 membrane glycoprotein CLA-1 precursor - human

N:Alternates: CD36 and LIMP-II analogous-1 (CLA-1)

N:Contains: membrane glycoprotein CLA-1, short splice form

C:Species: Homo sapiens (man)

C:Date: 07-Apr-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C:Accession: S36656; A48528

R:Vega, M.

Submitted to the BMBL Data Library, April 1993

A:Reference number: S36656

A:Accession: S36656

A:Molecule type: mRNA

A:Residues: 1-509 <VEG>

A:Cross references: UNIPROT:Q8WTV0; UNIPARC:UP10000073A04; EMBL:Z22255; NID:9197606; 1

A:Note: this sequence report represents the long form

R:Calvo, D.I. Vega, M.A.

J. Biol. Chem. 268, 18929-18935, 1993

A:Title: Identification, primary structure, and distribution of CLA-1, a novel member

A:Reference number: A48528

A:Accession: A48528

A:Molecule type: mRNA

A:Residues: 1-42143-509 <CAL>

A:Cross references: UNIPARC:UP10000174241; GB:Z22555

A;Note: this sequence report represents the short form; the long form was also sequenced
 C;Genetics:
 A;Gene: GDB:CD36L1
 A;Cross-references: GDB:228074
 A;MP Position: 12pter-12qter
 C;Superfamily: lysosomal membrane protein II
 C;Keywords: alternative splicing; blocked amino end; glycoprotein; lipoprotein; myristyl
 F:2-509/Product: membrane glycoprotein CLA-1, long splice form #status predicted <IMAT>
 F:2-8/Domain: intracellular #status predicted <CYT1>
 F:9-33/Domain: transmembrane #status predicted <TM1>
 F:443-464/Domain: extracellular #status predicted <TM2>
 F:465-509/Domain: transmembrane #status predicted <TM2>
 F:2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
 E:3/Binding site: palmitate (Cys) (covalent) #status predicted
 E:102,108,173,212,227,255,310,330/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 72.5%; Score 37; DB 1; Length 509;
 Best Local Similarity 75.0%; Pred. No. 28;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 YFPQQPAF 8
 Db 1.94 YFPGMFPF 201

RESULT 3
 DB2679 3
 A;Hypothetical protein XP1451 [imported] - *Xylella fastidiosa* (strain 9a5c)
 C;Species: *Xylella fastidiosa*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: D82679
 R;anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A;Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
 A;Reference number: A82515; PMID:20365717; PMID:10910347
 A;Note: For a complete list of authors see reference number A59328 below
 A;Accession: D82679
 A;Status: preliminary
 A;Molecule type: DNA
 A;Cross-references: UNIPROT:Q9DDC8 ; UNIPARC:UPI00000C272B ; GB:AE003975 ; GB:AE003849 ; NID
 R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarezaga, R.; Brion, P.; Bueno, M.R.P.; Camargo, A.A.; Canargo, L.B.A.; Carraro, D.M.; Carter, P.; de-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 Submitted to GenBank, June 2000
 A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froehl, J.; Gomes, M.L.; Kemper, B.L.; Kitajima, J.B.; Krieger, E.B.; Kuramitsu, S.; Laigus, F.; Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, P.; Authors: Martins, E.M.F.; Maeukuma, A.Y.; Menck, C.P.M.; Miracca, B.C.; Mizaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savasak
 A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tauhako, M.H.; Valada, R.; van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; 2
 A;Content: annotation
 C;Genetics:
 A;Gene: XE1451
 Query Match 72.5%; Score 37; DB 2; Length 636;
 Best Local Similarity 75.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 4
 G90388 4
 A;Thermopsine precursor related protein [imported] - *Sulfolobus solfataricus*
 C;Keywords: cAMP receptor protein cyclic nucleotide-binding domain homology <CA
 F:620-742/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CA
 Query Match 70.6%; Score 36; DB 2; Length 909;

C;Species: *Sulfolobus solfataricus*
 C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
 C;Accession: G90388
 R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Ch
 Jong, I.; Jeffries, A.C.; Fozena, C.J.; Medina, N.; Peng, X.; Thi-NGOC, H.P.; Redder
 arrest, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
 A;Description: *Sulfolobus solfataricus* complete genome.
 A;Reference number: A99139
 A;Accession: G90388
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-443 <KUR>
 A;Cross-references: UNIPROT:Q97WMO ; UNIPARC:UPI0000064687 ; GB:AE006641 ; NID:913815492
 C;Genetics:
 A;Gene: SS02194
 Query Match 70.6%; Score 36; DB 2; Length 443;
 Best Local Similarity 66.7%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 YFPQGAFS 9
 Db 342 YFPGNFTLS 350

RESULT 5
 SS0336 5
 hypothetical protein YMR140W - Yeast (Saccharomyces cerevisiae)
 N;Alternative names: hypothetical protein YMR375.09
 C;Species: *Saccharomyces cerevisiae*
 C;Date: 13-Jan-1995 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004
 C;Accession: S50396
 R;Baddock, K.; Churcher, C.
 Submitted to the EMBL Data library, December 1994
 A;Reference number: S50398
 A;Accession: S50396
 A;Molecule type: DNA
 A;Residues: 1-489 <BAD>
 A;Cross-references: UNIPROT:R40210 ; UNIPARC:UPI000013B8BA ; EMBL:Z47071 ; NID:9606429;
 C;Genetics:
 A;Gene: MIPS:YMR140W
 A;Cross-references: SGD:S0004748
 A;Map position: 13R
 Query Match 70.6%; Score 36; DB 2; Length 489;
 Best Local Similarity 66.7%; Pred. No. 42;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 YFPQGAFS 9
 Db 277 YFPGPFNYS 285

RESULT 6
 S32538 6
 CGMP-gated cation channel 2, rod - human
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S32538
 R;Chen, T.Y.; Peng, Y.W.; Dhallan, R.S.; Ahamed, B.; Reed, R.R.; Yau, K.W.
 Nature 362, 764-767, 1993
 A;Title: A new subunit of the cyclic nucleotide-gated cation channel in retinal rods.
 A;Reference number: S32538 ; MUID:93226050 ; PMID:7682292
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-909 <CHE>
 A;Cross-references: UNIPROT:043636 ; UNIPARC:UPI000017C0CA
 F:620-742/Domain: cAMP binding
 Query Match 70.6%; Score 36; DB 2; Length 909;

Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 9
Db	523 YFTGVFQF 531	Db	754 YKPGQFQF 762
RESULT 9			
AE2270	excinuclease ABC chain A <i>uvra</i> [imported] - <i>Nostoc</i> sp. (strain PCC 7120)	Qy	1 YFPQGFQF 9
C;Species: <i>Nostoc</i> sp. PCC 7120	N;Contains: 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12); proline dehydrogenase	Db	754 YKPGQFQF 762
A;Note: <i>Nostoc</i> sp. strain PCC 7120 is a synonym of <i>Anabaena</i> sp. strain PCC 7120	C;Species: <i>Escherichia coli</i>		
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001	C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004		
C;Accession: AR2270	C;Accession: U53597; S3126		
R.;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi	R.;Xia, M.; Zhu, Y.; Cao, X.; Chen, Z.		
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.	PEMS Microbiol. Lett. 127: 235-242, 1995		
DNA Res. 8: 205-213, 2001	A;Title: Cloning, sequencing and analysis of a gene encoding <i>Escherichia coli</i> proline		
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium <i>Anabaena</i> sp. strain PCC 7120	A;Reference number: U53597; MUID:95278725; PMID:7758938		
A;Accession: AR2270	A;Accession: U53597		
A;Status: preliminary	A;Status: translated from GB/EMBL/DBJ		
A;Residues: 1-361 <KUR>	A;Residues: 1-1310 <XIN>		
A;Cross-references: UNIPARC:Q8YQVO; UNIPARC:UPI000000CE8AA; GB:BA0000019; PIDN:BAB75415.1;	A;Cross-references: UNIPROT:Q59426; UNIPARC:UPI00000AE625; EMBL:X78340; NID:9467735;		
A;Experimental source: strain PCC 7120	A;Experimental source: strain K-12; substrain CSH4		
A;Gene: <i>uvra</i>	A;Gene: putA		
C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology	C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydrogenase		
A;Molecule type: DNA	C;Keywords: FAD; flavoprotein; NAD; oxidoreductase		
A;Cross-references: UNIPARC:1-361 <KUR>	C;Genetics:		
A;Experimental source: strain PCC 7120	A;Gene: putA		
C;Genetics:	F;87/Active site: Glu #status predicted		
A;Gene: <i>uvra</i>	F;91/Active site: Cys #status predicted		
C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology			
Query Match Score 70.6%; Best Local Similarity 66.7%; Matches 6; Conservative 2; Gaps 0;	Query Match Score 70.6%; Best Local Similarity 62.5%; Matches 5; Conservative 2; Gaps 0;		
Qy 1 YFPQGFQF 9	Qy 1 YFPQGFQF 8		
Db 739 YKPGQFQF 747	Db 500 YKPGQFQF 507		
		RESULT 10	
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 8			
S77349	excinuclease ABC chain A - <i>Synechocystis</i> sp. (strain PCC 6803)	Qy	1 YFPQGFQF 9
N;Contains: excinuclease ABC chain A	N;Alternate names: proline oxidase	Db	754 YKPGQFQF 762
C;Species: <i>Synechocystis</i> sp.	N;Contains: 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12); proline dehydrogenase		
A;Variety: PCC 6803	C;Species: <i>Escherichia coli</i>		
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004	C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004		
C;Accession: S77349	C;Accession: U53664; S313664; S07035		
R.;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O.; K.; Okamura, S.; Shimojo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda	R.;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; A.; Rose, D.J.; Mau, B.; Shao, Y.		
DNA Res. 3: 109-136, 1995	Science 277: 1453-1462, 1997		
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium <i>Synechocystis</i> sp.	A;Title: The complete genome sequence of <i>Escherichia coli</i> K-12.		
A;Accession: S74322; PMID:97061201; PMID:8905231	A;Accession: U53663		
A;Molecule type: DNA	A;Molecule type: DNA		
A;Residues: 1-970 <KAN>	A;Cross-references: UNIPROT:R09096; GB:AB001339; NII		
A;Cross-references: UNIPARC:P73412; UNIPARC:UPI000013789D; EMBL:D90906;	A;Status: nucleic acid sequence not shown; translation not shown		
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996	A;Accession: U53663		
C;Genetics:	A;Accession: S53365		
A;Gene: <i>uvra</i>	A;Molecule type: DNA		
C;Function: has ATPase and DNA binding activity; involved in DNA repair	A;Residues: 1-530; 'A', 532-1320 <LIN>		
C;Superfamily: excinuclease ABC chain A; ATP-binding cassette homology	A;Cross-references: UNIPARC:UPI0000168C4A; EMBL:U05212; NID:9468874; PIDN:ABB9985.1;		
C;Keywords: ATP; DNA binding; duplication; hydrolase; nucleotide binding; P- P;34-41/Region: nucleotide-binding motif A (P-loop)	A;Experimental source: strain K-12		
F;612-935/Domain: ATP-binding cassette homology <ABC>- F;659-676/Region: nucleotide-binding motif A (P-loop)	R.;Ling, M.; Allen, S.W.; Wood, J.M.		
Query Match Score 70.6%; Best Local Similarity 66.7%; Matches 6; Conservative 2; Gaps 0;	J. Mol. Biol. 243: 950-956, 1994		
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 9			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 9
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 10			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 11			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 12			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 13			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 14			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 15			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 16			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 17			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 18			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 19			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 20			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 21			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 22			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 23			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 24			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 25			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 26			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 27			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 28			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 29			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 30			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 31			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 32			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 33			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 34			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 35			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 36			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 37			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 38			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 39			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 40			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 41			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 42			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 43			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 44			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 45			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 46			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 47			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 48			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 49			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 50			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 51			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507
RESULT 52			
Qy	1 YFPQGFQF 9	Qy	1 YFPQGFQF 8
Db	754 YKPGQFQF 762	Db	500 YKPGQFQF 507

A;Cross-references: UNIPARC:UPI0000172085; UNIPARC:UPI0000172086; UNIPARC:UPI0000172087;
 P;Nakao, T.; Yanato, T.; Anraku, Y.
 B;Title: Nucleotide sequence of purC, the regulatory region for the put regulon of Escherichia coli. Genet. 210: 364-368, 1987
 P;Reference number: S06385; MUID:88142554; PMID:3325781
 A;Accession: S07035
 A;Molecule type: DNA
 A;Residues: 1-19, 'F', 21-40, 'AR', 43-44, 'GKQYSGAGATCAAFWR', <NAK>
 A;Cross-references: UNIPARC:UPI000172089; EMBL:X05653; NID:942599; PID:CAA29141.1; PID: A;Gene: putA; poAA
 A;Map position: <DPB>
 A;Function: <DPB>
 A;Description: EC 1.5.99.8 [validated, MUID:95055736]; transfers electrons from proline to proline
 A;Pathway: proline utilization
 A;Note: membrane-bound with proline
 C;Function: <PCD>
 A;Description: EC 1.5.1.12 [validated, MUID:95055736]; catalyzes the hydrolysis of 1-pyrrolin-5-carboxylate
 A;Pathway: proline utilization
 C;Function: <PRP>
 A;Description: controls the expression of the genes putP and putA in response to proline
 C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrrolin-5-carboxylate dehydrogenase
 C;Keywords: DNA binding; FAD; flavoprotein; membrane-associated protein; NAD; oxidoreductase
 P;883/Active site: Glu #status predicted
 P;917/Active site: Cys #status predicted
 Query Match Score 36; DB 1; Length 1320;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 0; Gaps 0;
 Qy 1 YFPGQFAF 8
 Db 503 YYPGQYEF 510

RESULT 11
 S66279
 Proline dehydrogenase (EC 1.5.99.8) / 1-pyrrolin-5-carboxylate dehydrogenase (EC 1.5.1.1).
 C;Species: *Salmonella typhimurium* [imported] - *Salmonella enterica* subsp. *enterica* serovar *Typhi*
 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: S66279; S33716; B3192; S03817; S31910
 R;Maloy, S. R.
 A;Reference number: S66279
 A;Accession: S66279
 A;Molecule type: DNA
 A;Residues: 1-1320 <MAL>
 A;Cross-references: UNIPROT:PI0503; UNIPARC:UPI00001703CD; EMBL:X70843; NID:g470179; PID: A;Experimental source: strain LT2
 A;Note: this is a revision to the sequence from reference S33716
 R;Allen, S. W.; Senti Willis, A.; Maloy, S. R.
 A;Title: DNA sequence of the putA gene from *Salmonella typhimurium*: a bifunctional membrane protein. Nucleic Acids Res. 21, 1676, 1993
 A;Reference number: S33716; MUID:93241961; PMID:8479928
 A;Accession: S33716
 A;Nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-19, 'WPRVSI', '28-272', 'ENWR', '278-279', 'SAILTICWAN', '290-368', 'APKRRIVWRSICKRSACYGRGRPAAPGICCRVYANLMMTR, <ALL>
 A;Cross-references: UNIPARC:UPI0000172082; EMBL:X70843
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1993
 R;Ling, M.; Allen, S. W.; Wood, J. M.
 J. Mol. Biol. 243, 930-956, 1994
 A;Contents: annotation
 R;Ostrovsky de Spicer, P.; O'Brien, K.; Maloy, S.
 J. Bacteriol. 173, 211-219, 1991
 A;Title: Regulation of proline utilization in *Salmonella typhimurium*: a membrane-associated protein. NID:90786
 A;Reference number: A39192; MUID:95055736; PMID:7966312
 A;Accession: B39192
 A;Status: preliminary

RESULT 12
 AE0633
 proline dehydrogenase (proline oxidase) [imported] - *Salmonella enterica* subsp. *enterica* serovar *Typhi*
 C;Species: *Salmonella enterica* subsp. *enterica* serovar *Typhi*
 A;Note: this species has also been called *Salmonella typhi*
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 15-Mar-2004
 C;Accession: AE0633
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church T.; Connor, P.; Cronin, A.; Davis, P.; Dowd, L.; White, N.; Farr S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar *Typhi* A;Accession: AB0502; MUID:1534937; PMID:1167708
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1320 <PAR>
 A;Cross-references: UNIPARC:UPI0000059F00; GB:AL513382; PIDN:CAD08246.1; PID:g1650225
 C;Genetics:
 A;Gene: STM1159
 C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrrolin-5-carboxylate dehydrogenase
 Query Match Score 36; DB 2; Length 1320;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Gaps 0;
 Qy 1 YFPGQFAF 8
 Db 503 YYPGQYEF 510

RESULT 13
 D90786
 proline dehydrogenase [imported] - *Escherichia coli* (strain O157:H7, substrate RIMD 25412569)
 C;Species: *Escherichia coli*

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: D9786
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Yokoyama, K.; Han, C.G.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: D90786
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-1320 <STO>
 A;Cross-references: UNIPARC:UPI0000165406; GB:BA0000007; PIDN:BA834683.1;
 A;Experimental source: strain O157:H7, substrate RIMD 0503952
 A;Gene: EC91260
 C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydr

Query Match 70.6%; Score 36; DB 2; Length 1320;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPQQQAF 8
 |:|||:
 Db 503 YYPGQYEF 510

RESULT 14

B85646
 proline dehydrogenase, PSC dehydrogenase [imported] - Escherichia coli (strain O157:H7,
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C;Accession: B85646
 R;Ferna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A854480; MUID:21074935; PMID:11206551
 A;Accession: B85646
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1320 <STO>
 A;Cross-references: UNIPARC:UPI000016575B; GB:AE0005174; NID:912514374; E
 A;Experimental source: strain O157:H7, substrate EDL933
 C;Genetics:
 A;Gene: putA
 C;Superfamily: bifunctional proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydr

Query Match 70.6%; Score 36; DB 2; Length 1320;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YFPQQQAF 8
 |:|||:
 Db 503 YYPGQYEF 510

RESULT 15

AB0225
 1-pyrroline-5-carboxylate dehydrogenase (EC 1.5.1.12) [imported] - Yersinia pestis (stra
 C;Species: Yersinia pestis
 C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AH0225
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
 ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
 Nature 413, 523-527, 2001
 A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A;Reference number: AB0001; MUID:21470413; PMID:11566360
 A;Accession: AH0225
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1323 <KTR>
 A;Cross-references: UNIPARC:UPI00000CD862; GB:AL590842; PIDN:CA90668.1;